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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:24:49 ; Search time 1371 Seconds
(without alignments)
34.495 Million cell updates/sec

Title: US-09-744-875-1
Perfect score: 21
Sequence: 1 agatttctaggaattcaaatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	21	AAZ92037	STAT5 binding sequ
	2	18	85.7	20	19	AAV46012	Immune adjuvant ST
	3	18	85.7	20	24	AAL39155	Murine Toll-like r
	4	18	85.7	100	22	AAA54479	DNA fragment compr
c	5	18	85.7	100	22	AAA54480	DNA fragment compr
	6	18	85.7	100	24	ABA93801	KZ134 plasmid cons
c	7	18	85.7	100	24	ABA93802	KZ134 plasmid cons
	8	18	85.7	100	24	AAS20691	Plasmid KZ 134 oli
c	9	18	85.7	100	24	AAS20692	Plasmid KZ 134 oli
	10	18	85.7	100	24	AAD22953	BaF3/KZ134/zalpha1
c	11	18	85.7	100	24	AAD22954	BaF3/KZ134/zalpha1
c	12	16	76.2	33	24	ABK88204	Human cytochrome b
	13	15.4	73.3	51	22	AAL31609	Human SNP oligonuc
c	14	14.8	70.5	41	24	ABL53039	Oligonucleotide JC
c	15	14.8	70.5	41	24	ABL53041	Oligonucleotide JC
c	16	14.8	70.5	44	24	ABL53037	Oligonucleotide JC
c	17	14.8	70.5	44	24	ABL53043	Oligonucleotide JC
c	18	14.6	69.5	46	20	AAZ23234	HCV NS5B gene ampl
	19	14.6	69.5	58	19	AAV59344	zsig10 primer ZC15
	20	14.6	69.5	58	20	AAX80718	Primer-5 for C-ter
	21	14.6	69.5	58	20	AAX24706	Linker primer ZC14
	22	14.6	69.5	58	22	AAS00972	PCR antisense comm
	23	14.6	69.5	58	24	ABN83120	Human alpha helica
	24	14.6	69.5	58	24	ABK12090	C-terminal-CEE-Zal
c	25	14.2	67.6	27	22	AAI64395	PCR primer #2. Un
c	26	14.2	67.6	27	22	AAI64405	PCR primer #12. U
c	27	14.2	67.6	51	22	AAI76494	Human silent SNP c
	28	14.2	67.6	61	21	AAC52964	Arabidopsis thalia
c	29	14.2	67.6	81	18	AAT86363	C. krusei non-tran
c	30	14	66.7	60	24	ABN41529	Human spliced tran
c	31	13.8	65.7	30	18	AAT58221	Candida CYB1 gene
c	32	13.8	65.7	30	19	AAV04870	PCR primer 2 used
c	33	13.8	65.7	30	21	AAZ08279	PCR primer-1 used
	34	13.8	65.7	60	24	ABN47639	Human spliced tran
c	35	13.8	65.7	65	24	ABN57384	Mouse spliced tran
c	36	13.6	64.8	22	13	AAQ32872	Human apolipoprote
	37	13.6	64.8	30	16	AAQ87051	Apolipoprotein E g
c	38	13.6	64.8	34	17	AAT28097	Probe 07L1 isolate
	39	13.6	64.8	37	15	AAQ73305	Mini-attTn7 primer
	40	13.6	64.8	37	16	AAQ86761	attTn7 amplificati
c	41	13.6	64.8	38	21	AAZ95731	Clostridium botuli
	42	13.6	64.8	40	21	AAC63106	Shiga-like toxin 1
	43	13.6	64.8	41	21	AAC63105	Shiga-like toxin 1
	44	13.6	64.8	42	21	AAC63104	Shiga-like toxin 1
	45	13.6	64.8	44	24	AAD29413	PCR primer to crea

ALIGNMENTS

RESULT 1
AAZ92037
ID AAZ92037 standard; DNA; 21 BP.
XX
AC AAZ92037;
XX
DT 08-JUN-2000 (first entry)
XX
DE STAT5 binding sequence oligonucleotide MGFe.
XX
KW STAT5 protein; signal transducer and activator of transcription 5;
KW protein binding sequence; transcription factor modulator; inhibitor;
KW malignant cell removal; proliferative malignancy; neoplastic disease;
KW immunological disorder; inflammatory disorder; therapy; ds.
XX
OS Synthetic.
XX
PN WO200006696-A2.
XX
PD 10-FEB-2000.
XX
PF 30-JUL-1999; 99WO-US17366.
XX
PR 30-JUL-1998; 98US-0094695.
XX
PA (UYSF-) UNIV SOUTH FLORIDA.
XX
PI Zuckerman KS, Liu RY;
XX
DR WPI; 2000-195281/17.
XX
PT Therapeutic agent for treating transcription factor-related illnesses

PT such as proliferative malignancies, comprises an oligonucleotide for
PT regulating transcription factor function -
XX
PS Claim 15; Page 34; 43pp; English.
XX
CC This sequence represents a STAT5 (signal transducer and activator of
CC transcription 5) protein binding sequence. The invention relates to a
CC therapeutic agent comprising an effective amount of an oligonucleotide
CC (I) for modulating the function of transcription factors and a
CC pharmaceutical acceptable carrier. The oligonucleotides can be used in a
CC method of removing malignant cells in vitro. The oligonucleotides can be
CC used in compositions to inhibit transcription factors in illnesses where
CC transcription factors play a role, especially proliferative malignancies,
CC neoplastic diseases, and immunological and inflammatory disorders.
XX
SQ Sequence 21 BP; 8 A; 3 C; 3 G; 7 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAAATC 21
||||||||||||||||||||||
Db 1 AGATTTCTAGGAATTCAAATC 21

RESULT 2
AAV46012
ID AAV46012 standard; DNA; 20 BP.
XX
AC AAV46012;
XX
DT 16-OCT-1998 (first entry)
XX
DE Immune adjuvant STAT5.
XX
KW Immune system; adjuvant; vaccine; cancer; prophylactic; pathogenicity;
KW modulator; tolerance; regulator; helper cell; antigen; immunoglobulin;
KW Ig class; autoimmune response; T-cell; B-cell; tumour; ss.
XX
OS Class Bacteria.
XX
PN EP855184-A1.
XX
PD 29-JUL-1998.
XX
PF 23-JAN-1997; 97EP-0101019.
XX
PR 23-JAN-1997; 97EP-0101019.
XX
PA (HEEG/) HEEG K.
PA (LIPF/) LIPFORD G B.
PA (WAGN/) WAGNER H.
XX
PI Heeg K, Lipford GB, Wagner H;
XX
DR WPI; 1998-389630/34.
XX
PT Antigenic composition comprises polynucleotide fragment and antigen
PT - used as vaccine to treat or prevent e.g. cancer or pathogen
PT infections and to modulate immune response e.g. tolerance break and
PT regulation of TH1/TH2 cells
XX
PS Example 5; Page 9; 28pp; English.
XX
CC AAV45993-V46019 are fragments of bacterial polynucleotides which are
CC used as immune adjuvants for inclusion into vaccines to treat cancer and
CC for prophylaxis and/or treatment of conditions caused by pathogenic
CC micro-organisms. The polynucleotide is used for modulation of an immune
CC response and the modulation is selected from the group break of
CC tolerance, regulation of TH1/TH2 helper cell responses, switch of Ig
CC classes, treatment of autoimmune responses and induction of tolerances.
CC DNA oligomers are used to enhance the reactivity of immune cells to
CC viral, bacterial and parasitic antigens, to break tolerance in anergic T
CC and B cells e.g. against tumour antigens, as adjuvants in vaccination
CC against tumour-defined antigens and immunostimulatory substances in an
CC immune response against tumours and to suppress immune reactions of the
CC innate and acquired immune system. The composition is inexpensive and
CC stable and does not cause lethal shock, which happens with prior art
CC bacterial sequences.
XX
SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 other;

Query Match 85.7%; Score 18; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAA 18
||||||||||||||||||
Db 1 AGATTTCTAGGAATTCAA 18

RESULT 3
AAL39155
ID AAL39155 standard; DNA; 20 BP.
XX
AC AAL39155;
XX
DT 05-SEP-2002 (first entry)
XX
DE Murine Toll-like receptor related CpG DNA SEQ ID No 30.
XX
KW Murine Toll-like receptor; TLR9; TLR7; TLR8; ISNA; ds.
XX
OS Unidentified.
XX
PN WO200222809-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US29229.
XX
PR 15-SEP-2000; 2000US-233075P.
PR 23-JAN-2001; 2001US-263657P.
PR 17-MAY-2001; 2001US-291726P.
PR 22-JUN-2001; 2001US-300210P.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Bauer S, Lipford G, Wagner H;
XX
DR WPI; 2002-393964/42.
XX
PT New isolated murine Toll-like receptor (TLR)9, TLR7, TLR8 polypeptides,
PT useful for identifying species specificity of immunostimulatory nucleic
PT acid and identifying immunostimulatory nucleic acids -
XX
PS Disclosure; Page 76; 195pp; English.
XX
CC The invention relates to isolated murine Toll-like receptors (TLR)9,
CC TLR7 and TLR8 polypeptides. These polypeptides comprise fully defined
CC sequences of 1032, 1050 or 1032 amino acids as given in specification, or
CC their fragments, where TLR9, TLR7 and TLR8 polypeptides or their
CC fragments have an amino acid sequence which is identical to human TLR9,
CC TLR7 or TLR8 polypeptides or their fragment except for at least one amino
CC acid of a murine TLR polypeptide. The isolated nucleic acids of the
CC invention are useful for inhibiting TLR9 signalling activity in a cell.
CC TLR7, TLR8 and TLR9 polypeptides are useful for identifying nucleic acid
CC molecules which interact with a TLR polypeptide or its fragment. The
CC TLR7, TLR8 or TLR9 polypeptides are also useful for identifying ISNA. The
CC TLR7, TLR8 and TLR9 polypeptides are also useful for comparing TLR9
CC signalling activity of a test compound (that is not a nucleic acid, and
CC is a polypeptide or a part of a combinatorial library of compounds) with
CC an ISNA. The TLR7, TLR8 and TLR9 polypeptides are also useful for
CC identifying species specificity of an ISNA. The isolated nucleic acids of
CC the invention are useful as probes or primers. This polynucleotide

CC sequence represents DNA relating to the isolated Toll-like receptors of
CC the invention.
XX
SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 other;

Query Match 85.7%; Score 18; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAA 18
||||||||||||||||||
Db 1 AGATTTCTAGGAATTCAA 18

RESULT 4
AAA54479
ID AAA54479 standard; DNA; 100 BP.
XX
AC AAA54479;
XX
DT 11-APR-2001 (first entry)
XX
DE DNA fragment comprising STAT transcription factors.
XX
KW zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
KW binding; detection; modulation; recombinant cell;
KW haematopoietic cell; lymphoid cell; myeloid cell; lymph;
KW immune system; blood; bone; inflammatory response; inflammation;
KW spleen; human; primer; ss.
XX
OS Synthetic.
XX
PN WO200068381-A1.
XX
PD 16-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US12924.
XX
PR 11-MAY-1999; 99US-0309861.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Foster DC, Hammond AK, Lok S;
XX
DR WPI; 2001-016096/02.
XX
PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
PT that stimulate proliferation or development of haematopoietic,
PT lymphoid and myeloid cells
XX
PS Example 19; Page 128; 134pp; English.
XX
CC Isolating a nucleotide which encodes the zcytor 10 cytokine
CC receptor enables the production of recombinant cells expressing the
CC receptor. Those cells can then be used to detect the presence of a
CC modulator of zcytor10 protein by culturing the cells in the presence
CC of a test ligand and comparing levels of activity of mouse zcytor10
CC in the presence and absence of the test sample. Similarly, detection
CC of zcytor10 receptor ligand within a test sample can be achieved.
CC The method comprising contacting a test sample containing an amino
CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC cytokine receptor and detecting the binding of the polypeptide to a
CC ligand in the sample. Specified peptide fragments of the zcytor 10
CC cytokine receptor and the methods described are used to identify
CC ligands that stimulate the proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC the cytokine receptor are useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders and for generating
CC antibodies directed against the receptor. An exemplary luciferase
CC mammalian expression vector is the KZ134 plasmid which was
CC constructed with two complementary oligonucleotides (AAA54479,
CC AAA54480) which comprise STAT transcription factors from 4 genes
CC (a modified c-fos Sis element, the p21 SIE1 from the p21 WAF1
CC gene, the mammary gland response element of the Beta-casein gene
CC and a STAT inducible element of the Fcg R1 gene.
XX
SQ Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;

Query Match 85.7%; Score 18; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAA 18
||||||||||||||||||
Db 67 AGATTTCTAGGAATTCAA 84

RESULT 5
AAA54480/c
ID AAA54480 standard; DNA; 100 BP.
XX
AC AAA54480;
XX
DT 11-APR-2001 (first entry)
XX
DE DNA fragment comprising STAT transcription factors.
XX
KW zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
KW binding; detection; modulation; recombinant cell;
KW haematopoietic cell; lymphoid cell; myeloid cell; lymph;
KW immune system; blood; bone; inflammatory response; inflammation;
KW spleen; human; primer; ss.
XX
OS Synthetic.
XX
PN WO200068381-A1.
XX
PD 16-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US12924.
XX
PR 11-MAY-1999; 99US-0309861.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Foster DC, Hammond AK, Lok S;
XX
DR WPI; 2001-016096/02.
XX
PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
PT that stimulate proliferation or development of haematopoietic,
PT lymphoid and myeloid cells
XX
PS Example 19; Page 128; 134pp; English.
XX
CC Isolating a nucleotide which encodes the zcytor 10 cytokine
CC receptor enables the production of recombinant cells expressing the
CC receptor. Those cells can then be used to detect the presence of a
CC modulator of zcytor10 protein by culturing the cells in the presence
CC of a test ligand and comparing levels of activity of mouse zcytor10
CC in the presence and absence of the test sample. Similarly, detection
CC of zcytor10 receptor ligand within a test sample can be achieved.
CC The method comprising contacting a test sample containing an amino
CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC cytokine receptor and detecting the binding of the polypeptide to a
CC ligand in the sample. Specified peptide fragments of the zcytor 10
CC cytokine receptor and the methods described are used to identify
CC ligands that stimulate the proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC the cytokine receptor are useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders and for generating
CC antibodies directed against the receptor. An exemplary luciferase
CC mammalian expression vector is the KZ134 plasmid which was
CC constructed with two complementary oligonucleotides (AAA54479,
CC AAA54480) which comprise STAT transcription factors from 4 genes
CC (a modified c-fos Sis element, the p21 SIE1 from the p21 WAF1

CC gene, the mammary gland response element of the Beta-casein gene
CC and a STAT inducible element of the Fcg R1 gene.
XX
SQ Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;

Query Match 85.7%; Score 18; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAA 18
||||||||||||||||||
Db 38 AGATTTCTAGGAATTCAA 21

RESULT 6
ABA93801
ID ABA93801 standard; DNA; 100 BP.
XX
AC ABA93801;
XX
DT 01-MAY-2002 (first entry)
XX
DE KZ134 plasmid construction oligonucleotide SEQ ID NO:43.
XX
KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease;
KW PCR primer; probe; ss.
XX
OS Synthetic.
XX
PN WO200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
PR 29-JUN-2000; 2000US-214955P.
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer MF;
XX
DR WPI; 2002-090519/12.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT spleenic, blood or bone disorders -
XX
PS Example 19; Page 190; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antirheumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, spleenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducting cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;

Query Match 85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAA 18
||||||||||||||||||
Db 67 AGATTTCTAGGAATTCAA 84

RESULT 7
ABA93802/c
ID ABA93802 standard; DNA; 100 BP.
XX
AC ABA93802;
XX
DT 01-MAY-2002 (first entry)
XX
DE KZ134 plasmid construction oligonucleotide SEQ ID NO:44.
XX
KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease;
KW PCR primer; probe; ss.
XX
OS Synthetic.
XX
PN WO200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
PR 29-JUN-2000; 2000US-214955P.
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer MF;
XX
DR WPI; 2002-090519/12.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT spleenic, blood or bone disorders -
XX
PS Example 19; Page 190; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antirheumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, spleenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducting cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;

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  Query Match            85.7%;  Score 18;  DB 24;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 8
AAS20691
ID   AAS20691 standard; DNA; 100 BP.
XX
AC   AAS20691;
XX
DT   09-APR-2002  (first entry)
XX
DE   Plasmid KZ 134 oligonucleotide ZC12749.
XX
KW   Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW   natural killer cell proliferation; T-cell proliferation;
KW   B-cell proliferation; anti-tumour response; immune system;
KW   immunostimulant; cytostatic; primer; ss.
XX
OS   Synthetic.
XX
PN   US6307024-B1.
XX
PD   23-OCT-2001.
XX
PF   09-MAR-2000; 2000US-0522217.
XX
PR   09-MAR-1999;   99US-123547P.
PR   11-MAR-1999;   99US-123904P.
PR   01-JUL-1999;   99US-142013P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Novak JE,  Presnell SR,  Sprecher CA,  Foster DC,  Holly RD,  Gross JA;
PI   Johnston JV,  Nelson AJ,  Dillon SR,  Hammond AK;
XX
DR   WPI; 2002-040208/05.
XX
PT   New zalpha11 ligand polypeptides and polynucleotides, useful for
PT   stimulating proliferation, activation, differentiation and/or induction
PT   of inhibition of specialized cell function, or for stimulating an
PT   antigenic response  -
XX
PS   Example 20; Column 149-150; 105pp; English.
XX
CC   The present invention relates to the isolation of a novel cytokine,
CC   zalpha11 Ligand and the polynucleotide encoding it. The invention
CC   also gives the sequence for the zalpha11 receptor and the polynucleotide
CC   encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC   natural killer (NK) cells or NK cell progenitors, the activation of NK
CC   cells, proliferation of T-cells, proliferation of B-cells stimulated
CC   with anti-CD40 antibodies, stimulates an antigenic response in a mammal,
CC   and reduces proliferation of B-cells stimulated with anti-IgM antibodies.
CC   The zalpha11 Ligand polypeptide is also useful in preparing antibodies
CC   that bind to zalpha11 Ligand epitopes. The zalpha11 Ligand
CC   polynucleotides can be used as probes or primers to clone regions
CC   of a zalpha11 Ligand gene, and in gene therapy. Zalpha11 Ligand may
CC   also be used to identify inhibitors of its activity, to enhance the
CC   generation of anti-tumour responses with or without the infusion of
CC   donor lymphocytes, and to activate or stimulate the immune system.
CC   The present sequence represents an oligonucleotide used to construct
CC   plasmid KZ 134 in the methods of the present invention.
XX
SQ   Sequence 100 BP; 25 A; 32 C; 17 G; 26 T; 0 other;

  Query Match            85.7%;  Score 18;  DB 24;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAA 84


RESULT 9
AAS20692/c
ID   AAS20692 standard; DNA; 100 BP.
XX
AC   AAS20692;
XX
DT   09-APR-2002  (first entry)
XX
DE   Plasmid KZ 134 oligonucleotide ZC12748.
XX
KW   Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW   natural killer cell proliferation; T-cell proliferation;
KW   B-cell proliferation; anti-tumour response; immune system;
KW   immunostimulant; cytostatic; primer; ss.
XX
OS   Synthetic.
XX
PN   US6307024-B1.
XX
PD   23-OCT-2001.
XX
PF   09-MAR-2000; 2000US-0522217.
XX
PR   09-MAR-1999;   99US-123547P.
PR   11-MAR-1999;   99US-123904P.
PR   01-JUL-1999;   99US-142013P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Novak JE,  Presnell SR,  Sprecher CA,  Foster DC,  Holly RD,  Gross JA;
PI   Johnston JV,  Nelson AJ,  Dillon SR,  Hammond AK;
XX
DR   WPI; 2002-040208/05.
XX
PT   New zalpha11 ligand polypeptides and polynucleotides, useful for
PT   stimulating proliferation, activation, differentiation and/or induction
PT   of inhibition of specialized cell function, or for stimulating an
PT   antigenic response  -
XX
PS   Example 20; Column 149-151; 105pp; English.
XX
CC   The present invention relates to the isolation of a novel cytokine,
CC   zalpha11 Ligand and the polynucleotide encoding it. The invention
CC   also gives the sequence for the zalpha11 receptor and the polynucleotide
CC   encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC   natural killer (NK) cells or NK cell progenitors, the activation of NK
CC   cells, proliferation of T-cells, proliferation of B-cells stimulated
CC   with anti-CD40 antibodies, stimulates an antigenic response in a mammal,
CC   and reduces proliferation of B-cells stimulated with anti-IgM antibodies.
CC   The zalpha11 Ligand polypeptide is also useful in preparing antibodies
CC   that bind to zalpha11 Ligand epitopes. The zalpha11 Ligand
CC   polynucleotides can be used as probes or primers to clone regions
CC   of a zalpha11 Ligand gene, and in gene therapy. Zalpha11 Ligand may
CC   also be used to identify inhibitors of its activity, to enhance the
CC   generation of anti-tumour responses with or without the infusion of
CC   donor lymphocytes, and to activate or stimulate the immune system.
CC   The present sequence represents an oligonucleotide used to construct
CC   plasmid KZ 134 in the methods of the present invention.
XX
SQ   Sequence 100 BP; 26 A; 17 C; 32 G; 25 T; 0 other;

  Query Match            85.7%;  Score 18;  DB 24;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 63;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
```

```
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 10
AAD22953
ID   AAD22953 standard; DNA; 100 BP.
XX
AC   AAD22953;
XX
DT   26-FEB-2002  (first entry)
XX
DE   BaF3/KZ134/zalpha11 cell line constructing ZC12,749 oligonucleotide.
XX
KW   Zalpha11; cytokine receptor; immunosuppressive; cytostatic; haemostatic;
KW   inflammatory disorder; cell proliferation; immune disorder; cancer; SLE;
KW   systemic lupus erythematosus; myasthenia gravis; rheumatoid arthritis;
KW   diabetes; autoimmune disease; multiple sclerosis; ulcerative colitis;
KW   inflammatory bowel disease; sepsis; Crohn's disease; viral infection;
KW   asthma; ss.
XX
OS   Unidentified.
XX
PN   WO200177171-A2.
XX
PD   18-OCT-2001.
XX
PF   03-APR-2001; 2001WO-US10872.
XX
PR   05-APR-2000; 2000US-194731P.
PR   28-JUL-2000; 2000US-222121P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sprecher CA,  Novak JE,  West JW,  Presnell SR,  Holly RD,  Nelson AJ;
XX
DR   WPI; 2002-025898/03.
XX
PT   Novel soluble receptor polypeptides and polynucleotides used as
PT   cytokine antagonist for stimulating ligand activity-induced
PT   proliferation of hematopoietic cells and for suppressing immune
PT   response in a mammal  -
XX
PS   Example 19; Page 213; 243pp; English.
XX
CC   The invention relates to an isolated soluble zalpha11 cytokine receptor
CC   polypeptide and their cDNA molecules. Zalpha proteins are useful for
CC   inhibiting or antagonising the ligand activity-induced proliferation of
CC   haematopoietic cells and haematopoietic cell progenitors preferably
CC   lymphoid cells which are natural killer cells or cytotoxic T cells.
CC   Zalpha is useful for treating immune and inflammatory disorders, for
CC   reducing proliferation of neoplastic B or T cells, for suppressing an
CC   immune response in a mammal exposed to an antigen or pathogen. Zalpha is
CC   useful for treating diseases that require immune regulation including
CC   autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC   myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC   asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC   sepsis, viral infection (dengue virus infection) and cancer. The present
CC   sequence is an oligonucleotide used for BaF3/KZ134/zalpha11 cell line
CC   construction.
XX
SQ   Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;

  Query Match             85.7%;  Score 18;  DB 24;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAA 84


RESULT 11
```

```
AAD22954/c
ID   AAD22954 standard; DNA; 100 BP.
XX
AC   AAD22954;
XX
DT   26-FEB-2002  (first entry)
XX
DE   BaF3/KZ134/zalpha11 cell line constructing ZC12,748 oligonucleotide.
XX
KW   Zalpha11; cytokine receptor; immunosuppressive; cytostatic; haemostatic;
KW   inflammatory disorder; cell proliferation; immune disorder; cancer; SLE;
KW   systemic lupus erythematosus; myasthenia gravis; rheumatoid arthritis;
KW   diabetes; autoimmune disease; multiple sclerosis; ulcerative colitis;
KW   inflammatory bowel disease; sepsis; Crohn's disease; viral infection;
KW   asthma; ss.
XX
OS   Unidentified.
XX
PN   WO200177171-A2.
XX
PD   18-OCT-2001.
XX
PF   03-APR-2001; 2001WO-US10872.
XX
PR   05-APR-2000; 2000US-194731P.
PR   28-JUL-2000; 2000US-222121P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sprecher CA,  Novak JE,  West JW,  Presnell SR,  Holly RD,  Nelson AJ;
XX
DR   WPI; 2002-025898/03.
XX
PT   Novel soluble receptor polypeptides and polynucleotides used as
PT   cytokine antagonist for stimulating ligand activity-induced
PT   proliferation of hematopoietic cells and for suppressing immune
PT   response in a mammal  -
XX
PS   Example 19; Page 213; 243pp; English.
XX
CC   The invention relates to an isolated soluble zalpha11 cytokine receptor
CC   polypeptide and their cDNA molecules. Zalpha proteins are useful for
CC   inhibiting or antagonising the ligand activity-induced proliferation of
CC   haematopoietic cells and haematopoietic cell progenitors preferably
CC   lymphoid cells which are natural killer cells or cytotoxic T cells.
CC   Zalpha is useful for treating immune and inflammatory disorders, for
CC   reducing proliferation of neoplastic B or T cells, for suppressing an
CC   immune response in a mammal exposed to an antigen or pathogen. Zalpha is
CC   useful for treating diseases that require immune regulation including
CC   autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC   myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC   asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC   sepsis, viral infection (dengue virus infection) and cancer. The present
CC   sequence is an oligonucleotide used for BaF3/KZ134/zalpha11 cell line
CC   construction.
XX
SQ   Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;

  Query Match             85.7%;  Score 18;  DB 24;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 12
ABK88204/c
ID   ABK88204 standard; DNA; 33 BP.
XX
AC   ABK88204;
XX
```

DT 07-OCT-2002 (first entry)
XX
DE Human cytochrome bcl core protein cDNA specific PCR primer #2.
XX
KW Cytochrome bcl; primer; ss; core protein II12. 21; cancer; HIV;
KW human immunodeficiency virus; human; PCR.
XX
OS Homo sapiens.
XX
PN CN1340524-A.
XX
PD 20-MAR-2002.
XX
PF 31-AUG-2000; 2000CN-0119831.
XX
PR 31-AUG-2000; 2000CN-0119831.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-436418/47.
XX
PT Polypeptide-human cytochrome bcl compound core protein II 12.21 and
PT polynucleotide for coding it -
XX
PS Example 4; Page 19 (disclosure); 34pp; Chinese.
XX
CC This invention relates to the cDNA and protein sequences of a novel
CC polypeptide-human cytochrome bcl compounds core protein II12. 21. The
CC invention also comprises a method for producing the protein by
CC recombinant DNA technology and a method for the application of the
CC polypeptide in treating diseases such as cancer, HIV infection, etc.
CC The invention also discloses an antagonist against this polypeptide and
CC its therapeutic action, and the application of the polynucleotide to
CC coding this new human cytochrome bcl compound core protein II12.21.
CC The present sequence represents a PCR primer used to clone the human
CC cytochrome bcl compound core protein II12.21 cDNA of the invention.
XX
SQ Sequence 33 BP; 10 A; 10 C; 4 G; 9 T; 0 other;

Query Match 76.2%; Score 16; DB 24; Length 33;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTC 16
||||||||||||||||
Db 19 AGATTTCTAGGAATTC 4

RESULT 13
AAL31609
ID AAL31609 standard; DNA; 51 BP.
XX
AC AAL31609;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #4817.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 2773; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 51 BP; 22 A; 6 C; 8 G; 15 T; 0 other;

Query Match 73.3%; Score 15.4; DB 22; Length 51;
Best Local Similarity 94.1%; Pred. No. 9.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATTTCTAGGAATTCAAA 19
||||||||||| |||||
Db 9 ATTTCTAGGAAGTCAAA 25

RESULT 14
ABL53039/c
ID ABL53039 standard; DNA; 41 BP.
XX
AC ABL53039;
XX
DT 29-MAY-2002 (first entry)
XX
DE Oligonucleotide JCA 325.
XX
KW Virucide; vaccine; foot and mouth disease; P1 region; capsid;
KW 3C protease; ds.
XX
OS Foot and mouth disease virus.
XX
PN WO200200251-A1.
XX
PD 03-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-FR02042.
XX
PR 29-JUN-2000; 2000FR-0008437.
XX
PA (MERI-) MERIAL.
XX
PI King A, Burman A, Audonnet J, Lombard M;

```
XX
DR   WPI; 2002-130837/17.
XX
PT   Stable, potent effective vaccines against foot-and-mouth disease,
PT   comprises recombinantly produced empty virus capsids as antigens  -
XX
PS   Example 7; Page 29; 79pp; French.
XX
CC   The present invention relates to a vaccine against foot and mouth disease
CC   (FMD) comprising (in addition to a veterinary vehicle or excipient) an
CC   antigen consisting of empty FMD virus capsids, obtained by expression in
CC   eukaryotic cells of the cDNA of the following regions of the FMD genome:
CC   the P1 region encoding the capsid and the region encoding the 3C
CC   protease. The vaccine is effective, reliable and stable, and is effective
CC   at low doses. The vaccine is useful against foot and mouth disease,
CC   especially in cows, sheep, pigs or goats. The present sequence is an
CC   oligonucleotide which was used in an example from the invention.
XX
SQ   Sequence 41 BP; 13 A; 7 C; 6 G; 15 T; 0 other;

  Query Match             70.5%;  Score 14.8;  DB 24;  Length 41;
  Best Local Similarity   88.9%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GATTTCTAGGAATTCAAA 19
           ||||| || |||||||||
Db      19 GATTTTTATGAATTCAAA 2


RESULT 15
ABL53041/c
ID   ABL53041 standard; DNA; 41 BP.
XX
AC   ABL53041;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Oligonucleotide JCA 327.
XX
KW   Virucide; vaccine; foot and mouth disease; P1 region; capsid;
KW   3C protease; ds.
XX
OS   Foot and mouth disease virus.
XX
PN   WO200200251-A1.
XX
PD   03-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-FR02042.
XX
PR   29-JUN-2000; 2000FR-0008437.
XX
PA   (MERI-) MERIAL.
XX
PI   King A,  Burman A,  Audonnet J,  Lombard M;
XX
DR   WPI; 2002-130837/17.
XX
PT   Stable, potent effective vaccines against foot-and-mouth disease,
PT   comprises recombinantly produced empty virus capsids as antigens  -
XX
PS   Example 7; Page 30; 79pp; French.
XX
CC   The present invention relates to a vaccine against foot and mouth disease
CC   (FMD) comprising (in addition to a veterinary vehicle or excipient) an
CC   antigen consisting of empty FMD virus capsids, obtained by expression in
CC   eukaryotic cells of the cDNA of the following regions of the FMD genome:
CC   the P1 region encoding the capsid and the region encoding the 3C
CC   protease. The vaccine is effective, reliable and stable, and is effective
CC   at low doses. The vaccine is useful against foot and mouth disease,
CC   especially in cows, sheep, pigs or goats. The present sequence is an
CC   oligonucleotide which was used in an example from the invention.
XX
SQ   Sequence 41 BP; 13 A; 6 C; 6 G; 16 T; 0 other;

  Query Match             70.5%;  Score 14.8;  DB 24;  Length 41;
  Best Local Similarity   88.9%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GATTTCTAGGAATTCAAA 19
           ||||| || |||||||||
Db      19 GATTTTTATGAATTCAAA 2


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Job time : 1375 secs
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 12:59:50 ; Search time 2684 Seconds
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Title: SCHMIDT875
Perfect score: 9
Sequence: 1 ttcnnngaa 9

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Searched: 2054640 seqs, 14551402878 residues

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Listing first 45 summaries

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2: gb_htg:*
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15: em_ba:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		6	66.7	9	6	AX041991	AX041991 Sequence
2	c	6	66.7	9	6	AX041991	AX041991 Sequence
3		6	66.7	9	6	AX058974	AX058974 Sequence
4	c	6	66.7	9	6	AX058974	AX058974 Sequence
5		6	66.7	9	6	BD012767	BD012767 Agent for
6	c	6	66.7	9	6	BD012767	BD012767 Agent for
7		6	66.7	10	6	AR043682	AR043682 Sequence
8	c	6	66.7	10	6	AR043682	AR043682 Sequence
9		6	66.7	10	6	AR043683	AR043683 Sequence
10	c	6	66.7	10	6	AR043683	AR043683 Sequence
11		6	66.7	10	6	AX301514	AX301514 Sequence
12	c	6	66.7	10	6	AX301514	AX301514 Sequence
13		6	66.7	10	6	AX301563	AX301563 Sequence
14	c	6	66.7	10	6	AX301563	AX301563 Sequence
15		6	66.7	11	6	A92561	A92561 Sequence 2
16	c	6	66.7	11	6	A92561	A92561 Sequence 2
17		6	66.7	11	6	AR171056	AR171056 Sequence
18	c	6	66.7	11	6	AR171056	AR171056 Sequence
19		6	66.7	11	6	AR171059	AR171059 Sequence
20	c	6	66.7	11	6	AR171059	AR171059 Sequence
21		6	66.7	11	6	AX063653	AX063653 Sequence
22	c	6	66.7	11	6	AX063653	AX063653 Sequence
23		6	66.7	11	6	AX063656	AX063656 Sequence
24	c	6	66.7	11	6	AX063656	AX063656 Sequence
25		6	66.7	11	6	AX470574	AX470574 Sequence
26	c	6	66.7	11	6	AX470574	AX470574 Sequence
27		6	66.7	11	6	AX470746	AX470746 Sequence
28	c	6	66.7	11	6	AX470746	AX470746 Sequence
29		6	66.7	11	6	I39714	I39714 Sequence 1
30	c	6	66.7	11	6	I39714	I39714 Sequence 1
31		6	66.7	11	6	I39715	I39715 Sequence 2
32	c	6	66.7	11	6	I39715	I39715 Sequence 2
33		6	66.7	11	6	I39722	I39722 Sequence 9
34	c	6	66.7	11	6	I39722	I39722 Sequence 9
35		6	66.7	11	6	I55831	I55831 Sequence 1
36	c	6	66.7	11	6	I55831	I55831 Sequence 1
37		6	66.7	11	6	I55832	I55832 Sequence 2
38	c	6	66.7	11	6	I55832	I55832 Sequence 2
39		6	66.7	11	6	I55839	I55839 Sequence 9
40	c	6	66.7	11	6	I55839	I55839 Sequence 9
41		6	66.7	12	6	AR171057	AR171057 Sequence
42	c	6	66.7	12	6	AR171057	AR171057 Sequence
43		6	66.7	12	6	AR171058	AR171058 Sequence
44	c	6	66.7	12	6	AR171058	AR171058 Sequence
45		6	66.7	12	6	AX063654	AX063654 Sequence

ALIGNMENTS

RESULT 1
AX041991
LOCUS AX041991 9 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 21 from Patent WO0065067.
ACCESSION AX041991
VERSION AX041991.1 GI:11340784
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9)
AUTHORS Nelson,P.S., Hood,L. and Lin,B.
TITLE Prostate-specific polynucleotides, polypeptides and their methods of use

```
  JOURNAL   Patent: WO 0065067-A 21 02-NOV-2000;
            The University of Washington (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     protein_bind    1. .9
                     /bound_moiety="Interleukin response element binding site"
BASE COUNT        3 a      3 c      1 g      2 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+09;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCCCAGAA 9


RESULT 2
AX041991/c
LOCUS       AX041991                  9 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 21 from Patent WO0065067.
ACCESSION   AX041991
VERSION     AX041991.1  GI:11340754
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Nelson,P.S., Hood,L. and Lin,B.
  TITLE     Prostate-specific polynucleotides, polypeptides and their methods
            of use
  JOURNAL   Patent: WO 0065067-A 21 02-NOV-2000;
            The University of Washington (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     protein_bind    1. .9
                     /bound_moiety="Interleukin response element binding site"
BASE COUNT        3 a      3 c      1 g      2 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+09;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCTGGGAA 1


RESULT 3
AX058974
LOCUS       AX058974                  9 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 13 from Patent WO0075326.
ACCESSION   AX058974
VERSION     AX058974.1  GI:12311244
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Auernhammer,C.J. and Shlomo,M.
  TITLE     Suppressor of cytokine signaling (socs)-3 promoter and methods for
            its use
  JOURNAL   Patent: WO 0075326-A 13 14-DEC-2000;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT        3 a      2 c      2 g      2 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+09;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCCAGGAA 9


RESULT 4
AX058974/c
LOCUS       AX058974                  9 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 13 from Patent WO0075326.
ACCESSION   AX058974
VERSION     AX058974.1  GI:12311244
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Auernhammer,C.J. and Shlomo,M.
  TITLE     Suppressor of cytokine signaling (socs)-3 promoter and methods for
            its use
  JOURNAL   Patent: WO 0075326-A 13 14-DEC-2000;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT        3 a      2 c      2 g      2 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+09;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCCTGGAA 1


RESULT 5
BD012767
LOCUS       BD012767                  9 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  Agent for enhancing expression of HM1.24 antigen.
ACCESSION   BD012767
VERSION     BD012767.1  GI:22092956
KEYWORDS    WO 0113940-A/8.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Kosaka,M., Ozaki,S. and Wakahara,Y.
  TITLE     Agent for enhancing expression of HM1.24 antigen
  JOURNAL   Patent: WO 0113940-A 8 01-MAR-2001;
            CHUGAI PHARMACEUTICAL CO LTD,MASAAKI KOSAKA,SHUJI OZAKI, UJI
            WAKAHARA
COMMENT     OS   Artificial Sequence
            PN   WO 0113940-A/8
            PD   01-MAR-2001
            PF   22-AUG-2000 WO 2000JP005617
            PR   23-AUG-1999 JP 99P   236007,16-FEB-2000 JP 00P   038689 PI
            MASAAKI KOSAKA,SHUJI OZAKI,YUJI WAKAHARA
            PC   A61K38/21,A61K39/395,A61K45/00,A61P35/00,A61P19/00,G01N33/50,
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            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      3 c      1 g      2 t
ORIGIN

  Query Match            66.7%;  Score 6;  DB 6;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 3.2e+09;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCCCAGAA 9


RESULT 6
BD012767/c
LOCUS       BD012767                 9 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  Agent for enhancing expression of HM1.24 antigen.
ACCESSION   BD012767
VERSION     BD012767.1  GI:22092956
KEYWORDS    WO 0113940-A/8.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Kosaka,M., Ozaki,S. and Wakahara,T.
  TITLE     Agent for enhancing expression of HM1.24 antigen
  JOURNAL   Patent: WO 0113940-A 8 01-MAR-2001;
            CHUGAI PHARMACEUTICAL CO LTD,MASAAKI KOSAKA,SHUJI OZAKI, UJI
            WAKAHARA
COMMENT     OS   Artificial Sequence
            PN   WO 0113940-A/8
            PD   01-MAR-2001
            PF   22-AUG-2000 WO 2000JP005617
            PR   23-AUG-1999 JP 99P   236007,16-FEB-2000 JP 00P   038689 PI
            MASAAKI KOSAKA,SHUJI OZAKI,YUJI WAKAHARA
            PC   A61K38/21,A61K39/395,A61K45/00,A61P35/00,A61P19/00,G01N33/50,
            PC   G01N33/15
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      3 c      1 g      2 t
ORIGIN

  Query Match            66.7%;  Score 6;  DB 6;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 3.2e+09;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCTGGGAA 1


RESULT 7
AR043682
LOCUS       AR043682                10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 52 from patent US 5814517.
ACCESSION   AR043682
VERSION     AR043682.1  GI:5964690
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 52 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        2 a      4 c      1 g      3 t
ORIGIN

  Query Match            66.7%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      2 TTCCCCGAA 10


RESULT 8
AR043682/c
LOCUS       AR043682                10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 52 from patent US 5814517.
ACCESSION   AR043682
VERSION     AR043682.1  GI:5964690
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 52 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        2 a      4 c      1 g      3 t
ORIGIN

  Query Match            66.7%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db     10 TTCGGGGAA 2


RESULT 9
AR043683
LOCUS       AR043683                10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 53 from patent US 5814517.
ACCESSION   AR043683
VERSION     AR043683.1  GI:5964691
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 53 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        4 a      1 c      1 g      4 t
ORIGIN

  Query Match            66.7%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
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Db      2 TTCTAAGAA 10


RESULT 10
AR043683/c
LOCUS       AR043683                 10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 53 from patent US 5814517.
ACCESSION   AR043683
VERSION     AR043683.1  GI:5964691
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 53 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
BASE COUNT        4 a      1 c      1 g      4 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db     10 TTCTTAGAA 2


RESULT 11
AX301514
LOCUS       AX301514                 10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 228 from Patent WO0185941.
ACCESSION   AX301514
VERSION     AX301514.1  GI:17382597
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 228 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      1 c      2 g      5 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCTGTGAA 9


RESULT 12
AX301514/c
LOCUS       AX301514                 10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 228 from Patent WO0185941.
ACCESSION   AX301514
VERSION     AX301514.1  GI:17382597
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 228 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      1 c      2 g      5 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCACAGAA 1


RESULT 13
AX301563
LOCUS       AX301563                 10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 277 from Patent WO0185941.
ACCESSION   AX301563
VERSION     AX301563.1  GI:17382646
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 277 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      1 c      2 g      5 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCTGTGAA 9


RESULT 14
AX301563/c
LOCUS       AX301563                 10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 277 from Patent WO0185941.
ACCESSION   AX301563
VERSION     AX301563.1  GI:17382646
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 277 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
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     source          1. .10
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      1 c      2 g      5 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       9 TTCACAGAA 1


RESULT 15
A92561
LOCUS       A92561                    11 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 2 from Patent WO9812320.
ACCESSION   A92561
VERSION     A92561.1  GI:6741220
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Stoecklin,E. and Groner,B.
  TITLE     NUCLEIC ACID CONSTRUCT CODING FOR A PROTEIN COMPLEX FROM A STAT
            PROTEIN AND A NUCLEAR RECEPTOR AND ITS USE
  JOURNAL   Patent: WO 9812320-A 2 26-MAR-1998;
            STOECKLIN ELISABETH (CH); GRONER BERND (CH)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      2 c      2 g      4 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 6;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 2.3e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       3 TTCTTGGAA 11


Search completed: December 25, 2002, 22:44:35
Job time : 2686 secs
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:24:49 ; Search time 3892 Seconds
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157.030 Million cell updates/sec

Title: US-09-744-875-1
Perfect score: 21
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Scoring table: IDENTITY_NUC
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Searched: 2054640 seqs, 14551402878 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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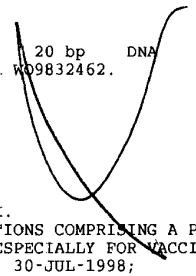
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		18	85.7	20	6	A89799	A89799 Sequence 21
2		18	85.7	20	6	A90886	A90886 Sequence 21
3		18	85.7	20	6	AX455553	AX455553 Sequence
4		18	85.7	21	6	I23456	I23456 Sequence 8
5		18	85.7	100	6	AR174601	AR174601 Sequence
6	c	18	85.7	100	6	AR174602	AR174602 Sequence
7		18	85.7	100	6	AX047032	AX047032 Sequence
8	c	18	85.7	100	6	AX047033	AX047033 Sequence
9		18	85.7	100	6	AX280202	AX280202 Sequence
10	c	18	85.7	100	6	AX280203	AX280203 Sequence
11		18	85.7	100	6	AX365191	AX365191 Sequence
12	c	18	85.7	100	6	AX365192	AX365192 Sequence
13	c	14.8	70.5	41	6	AX343814	AX343814 Sequence
14	c	14.8	70.5	41	6	AX343816	AX343816 Sequence
15	c	14.8	70.5	44	6	AX343812	AX343812 Sequence
16	c	14.8	70.5	44	6	AX343818	AX343818 Sequence
17		14.6	69.5	58	6	AR138229	AR138229 Sequence
18		14.6	69.5	58	6	AR140194	AR140194 Sequence
19		14.6	69.5	58	6	AR173275	AR173275 Sequence
20	c	14.6	69.5	82	3	AY096258	AY096258 Aurelia a
21	c	14.2	67.6	51	6	AX160107	AX160107 Sequence
22	c	14.2	67.6	76	8	YSCGENC152	M87429 Yeast Eco R
23	c	14.2	67.6	81	6	A65654	A65654 Sequence 3
24		14.2	67.6	82	3	S47134S1	S47134 Caenorhabdi
25	c	13.8	65.7	24	6	A03717	A03717 Oligonucleo
26	c	13.8	65.7	30	6	AR037059	AR037059 Sequence
27		13.8	65.7	91	1	AF087321	AF087321 Chlamydia
28		13.8	65.7	94	10	AY041972	AY041972 Phodopus
29	c	13.6	64.8	22	6	E03991	E03991 PCR primer
30	c	13.6	64.8	34	6	AR003332	AR003332 Sequence
31		13.6	64.8	37	6	A72766	A72766 Sequence 1
32		13.6	64.8	40	6	AR136808	AR136808 Sequence
33		13.6	64.8	40	6	BD000581	BD000581 Amplifica
34		13.6	64.8	40	6	I36897	I36897 Sequence 4
35		13.6	64.8	41	6	AR136807	AR136807 Sequence
36		13.6	64.8	41	6	BD000580	BD000580 Amplifica
37		13.6	64.8	42	6	AR136806	AR136806 Sequence
38		13.6	64.8	42	6	BD000579	BD000579 Amplifica
39		13.6	64.8	44	6	AX382229	AX382229 Sequence
40		13.6	64.8	68	6	A07635	A07635 DNA sequenc
41	c	13.4	63.8	28	6	AX455442	AX455442 Sequence
42		13.4	63.8	30	6	AR101803	AR101803 Sequence
43		13.4	63.8	30	6	AR173975	AR173975 Sequence
44	c	13.2	62.9	25	6	AR139827	AR139827 Sequence
45	c	13.2	62.9	25	6	AR167471	AR167471 Sequence

ALIGNMENTS

RESULT 1
A89799
LOCUS A89799 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 21 from Patent WO9832462.
ACCESSION A89799
VERSION A89799.1 GI:6738313
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 21 30-JUL-1998;



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            LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32644"
BASE COUNT        7 a      3 c      3 g      7 t
ORIGIN

  Query Match             85.7%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db      1 AGATTTCTAGGAATTCAA 18


RESULT 2
A90886
LOCUS       A90886                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 21 from Patent EP0855184.
ACCESSION   A90886
VERSION     A90886.1  GI:6739328
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 21 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      3 c      3 g      7 t
ORIGIN

  Query Match             85.7%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
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Db      1 AGATTTCTAGGAATTCAA 18


RESULT 3
AX455553
LOCUS       AX455553                 20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 30 from Patent WO0222809.
ACCESSION   AX455553
VERSION     AX455553.1  GI:21714621
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,S., Lipford,G. and Wagner,H.
  TITLE     Process for high throughput screening of cpg-based
            immuno-agonist/antagonist
  JOURNAL   Patent: WO 0222809-A 30 21-MAR-2002;
            Coley Pharmaceutical GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
BASE COUNT        7 a      3 c      3 g      7 t
ORIGIN
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  Query Match             85.7%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db      1 AGATTTCTAGGAATTCAA 18


RESULT 4
I23456
LOCUS       I23456                   21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 8 from patent US 5534409.
ACCESSION   I23456
VERSION     I23456.1  GI:1603326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Groner,B., Gouilleux,F. and Wakao,H.
  TITLE     Cytokine regulated transcription factor
  JOURNAL   Patent: US 5534409-A 8 09-JUL-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        7 a      4 c      3 g      7 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db      1 AGATTTCTAGGAATTCAA 18


RESULT 5
AR174601
LOCUS       AR174601                100 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 59 from patent US 6307024.
ACCESSION   AR174601
VERSION     AR174601.1  GI:17914921
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 59 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="unknown"
BASE COUNT       25 a     32 c     17 g     26 t
ORIGIN

  Query Match             85.7%;  Score 18;  DB 6;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
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Db     67 AGATTTCTAGGAATTCAA 84


RESULT 6
AR174602/c
LOCUS       AR174602                100 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 60 from patent US 6307024.
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ACCESSION   AR174602
VERSION     AR174602.1  GI:17914922
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 60 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="unknown"
BASE COUNT       26 a     17 c     32 g     25 t
ORIGIN

  Query Match           85.7%;  Score 18;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 7
AX047032
LOCUS       AX047032                100 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 37 from Patent WO0068381.
ACCESSION   AX047032
VERSION     AX047032.1  GI:11876456
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
  TITLE     Cytokine receptor mouse zcytor10
  JOURNAL   Patent: WO 0068381-A 37 16-NOV-2000;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12749"
BASE COUNT       24 a     33 c     17 g     26 t
ORIGIN

  Query Match           85.7%;  Score 18;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAA 84


RESULT 8
AX047033/c
LOCUS       AX047033                100 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 38 from Patent WO0068381.
ACCESSION   AX047033
VERSION     AX047033.1  GI:11876457
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Presnell,S.R., Foster,D.C., Hammond,A.K. and Lok,S.
  TITLE     Cytokine receptor mouse zcytor10
  JOURNAL   Patent: WO 0068381-A 38 16-NOV-2000;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12748"
BASE COUNT       26 a     17 c     33 g     24 t
ORIGIN

  Query Match           85.7%;  Score 18;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 9
AX280202
LOCUS       AX280202                100 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 48 from Patent WO0177171.
ACCESSION   AX280202
VERSION     AX280202.1  GI:16607595
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Novak,J.E., West,J.W., Presnell,S.R., Holly,R.D. and
            Nelson,A.J.
  TITLE     Soluble zalpha11 cytokine receptors
  JOURNAL   Patent: WO 0177171-A 48 18-OCT-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12749"
BASE COUNT       24 a     33 c     17 g     26 t
ORIGIN

  Query Match           85.7%;  Score 18;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAA 84


RESULT 10
AX280203/c
LOCUS       AX280203                100 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 49 from Patent WO0177171.
ACCESSION   AX280203
VERSION     AX280203.1  GI:16607596
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Novak,J.E., West,J.W., Presnell,S.R., Holly,R.D. and
            Nelson,A.J.
  TITLE     Soluble zalpha11 cytokine receptors
  JOURNAL   Patent: WO 0177171-A 49 18-OCT-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
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                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12748"
BASE COUNT       26 a     17 c     33 g     24 t
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ORIGIN

  Query Match            85.7%;  Score 18;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 11
AX365191
LOCUS       AX365191                  100 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 43 from Patent WO0200721.
ACCESSION   AX365191
VERSION     AX365191.1  GI:18696947
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuijper,J.L.
            and Maurer,M.F.
  TITLE     Cytokine receptor zcytor17
  JOURNAL   Patent: WO 0200721-A 43 03-JAN-2002;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12749"
BASE COUNT       24 a     38 c     17 g     26 t
ORIGIN

  Query Match            85.7%;  Score 18;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAA 84


RESULT 12
AX365192/c
LOCUS       AX365192                  100 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 44 from Patent WO0200721.
ACCESSION   AX365192
VERSION     AX365192.1  GI:18696948
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuijper,J.L.
            and Maurer,M.F.
  TITLE     Cytokine receptor zcytor17
  JOURNAL   Patent: WO 0200721-A 44 03-JAN-2002;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .100
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                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12748"
BASE COUNT       26 a     17 c     33 g     24 t
ORIGIN

  Query Match            85.7%;  Score 18;  DB 6;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 13
AX343814/c
LOCUS       AX343814                  41 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 21 from Patent WO0200251.
ACCESSION   AX343814
VERSION     AX343814.1  GI:18491887
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   King,A., Burman,A., Audonnet,J.C. and Lombard,M.
  TITLE     Vaccine against foot-and-mouth disease
  JOURNAL   Patent: WO 0200251-A 21 03-JAN-2002;
            MERIAL (FR)
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="synthetic construct"
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                     /note="oligonucleotide"
BASE COUNT       13 a      7 c      6 g     15 t
ORIGIN

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  Best Local Similarity  88.9%;  Pred. No. 1.1e+05;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 GATTTCTAGGAATTCAAA 19
          ||||| || |||||||||
Db     19 GATTTTTATGAATTCAAA 2


RESULT 14
AX343816/c
LOCUS       AX343816                  41 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 23 from Patent WO0200251.
ACCESSION   AX343816
VERSION     AX343816.1  GI:18491889
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   King,A., Burman,A., Audonnet,J.C. and Lombard,M.
  TITLE     Vaccine against foot-and-mouth disease
  JOURNAL   Patent: WO 0200251-A 23 03-JAN-2002;
            MERIAL (FR)
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT       13 a      6 c      6 g     16 t
ORIGIN

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  Best Local Similarity  88.9%;  Pred. No. 1.1e+05;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 GATTTCTAGGAATTCAAA 19
          ||||| || |||||||||
Db     19 GATTTTTATGAATTCAAA 2


RESULT 15
AX343812/c
LOCUS       AX343812                  44 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 19 from Patent WO0200251.
ACCESSION   AX343812
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VERSION     AX343812.1  GI:18491885
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   King,A., Burman,A., Audonnet,J.C. and Lombard,M.
  TITLE     Vaccine against foot-and-mouth disease
  JOURNAL   Patent: WO 0200251-A 19 03-JAN-2002;
            MERIAL (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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BASE COUNT       13 a        7 c        7 g       17 t
ORIGIN

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  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GATTTCTAGGAATTCAAA 19
           ||||| || ||||||||||
Db      19 GATTTTTATGAATTCAAA 2


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Job time : 3901 secs
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:40:44 ; Search time 52 Seconds
(without alignments)
53.079 Million cell updates/sec

Title: SCHMIDT875
Perfect score: 9
Sequence: 1 ttcnnngaa 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	6	66.7	9	1	US-08-411-020-10	Sequence 10, Appl
c	4	6	66.7	9	1	US-08-411-020-10	Sequence 10, Appl
	5	6	66.7	9	1	US-08-411-020-11	Sequence 11, Appl
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	7	6	66.7	9	1	US-08-411-020-12	Sequence 12, Appl
c	8	6	66.7	9	1	US-08-411-020-12	Sequence 12, Appl
	9	6	66.7	9	1	US-08-411-020-13	Sequence 13, Appl
c	10	6	66.7	9	1	US-08-411-020-13	Sequence 13, Appl
	11	6	66.7	9	1	US-08-369-796-25	Sequence 25, Appl
c	12	6	66.7	9	1	US-08-369-796-25	Sequence 25, Appl
	13	6	66.7	9	1	US-08-369-796-26	Sequence 26, Appl
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	15	6	66.7	9	1	US-08-369-796-27	Sequence 27, Appl
c	16	6	66.7	9	1	US-08-369-796-27	Sequence 27, Appl
	17	6	66.7	9	1	US-08-369-796-31	Sequence 31, Appl
c	18	6	66.7	9	1	US-08-369-796-31	Sequence 31, Appl
	19	6	66.7	9	1	US-08-369-796-34	Sequence 34, Appl
c	20	6	66.7	9	1	US-08-369-796-34	Sequence 34, Appl
	21	6	66.7	9	1	US-08-369-796-35	Sequence 35, Appl
c	22	6	66.7	9	1	US-08-369-796-35	Sequence 35, Appl
	23	6	66.7	9	1	US-08-369-796-36	Sequence 36, Appl
c	24	6	66.7	9	1	US-08-369-796-36	Sequence 36, Appl
	25	6	66.7	9	1	US-08-369-796-38	Sequence 38, Appl
c	26	6	66.7	9	1	US-08-369-796-38	Sequence 38, Appl
	27	6	66.7	9	1	US-08-410-779B-6	Sequence 6, Appli
c	28	6	66.7	9	1	US-08-410-779B-6	Sequence 6, Appli
	29	6	66.7	9	1	US-08-410-779B-23	Sequence 23, Appl
c	30	6	66.7	9	1	US-08-410-779B-23	Sequence 23, Appl
	31	6	66.7	9	1	US-08-410-779B-26	Sequence 26, Appl
c	32	6	66.7	9	1	US-08-410-779B-26	Sequence 26, Appl
	33	6	66.7	9	1	US-08-410-779B-28	Sequence 28, Appl
c	34	6	66.7	9	1	US-08-410-779B-28	Sequence 28, Appl
	35	6	66.7	9	1	US-08-410-779B-31	Sequence 31, Appl
c	36	6	66.7	9	1	US-08-410-779B-31	Sequence 31, Appl
	37	6	66.7	9	1	US-08-410-779B-33	Sequence 33, Appl
c	38	6	66.7	9	1	US-08-410-779B-33	Sequence 33, Appl
	39	6	66.7	9	1	US-08-410-779B-35	Sequence 35, Appl
c	40	6	66.7	9	1	US-08-410-779B-35	Sequence 35, Appl
	41	6	66.7	9	1	US-08-410-779B-51	Sequence 51, Appl
c	42	6	66.7	9	1	US-08-410-779B-51	Sequence 51, Appl
	43	6	66.7	9	2	US-08-852-091-25	Sequence 25, Appl
c	44	6	66.7	9	2	US-08-852-091-25	Sequence 25, Appl
	45	6	66.7	9	2	US-08-852-091-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-411-020-1
; Sequence 1, Application US/08411020
; Patent No. 5712094
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; APPLICANT: CHAN, SHIN-SHAY TIAN
; TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
; TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ligand Pharmaceuticals Incorporated
; STREET: 9393 Towne Centre Drive
; CITY: San Diego
; STATE: California
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,020
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jurgensen, Thomas E.
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0030.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
US-08-411-020-1

Query Match 66.7%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCNNNGAA 9

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Db      1 TTCNNNGAA 9


RESULT 2
US-08-411-020-1/c
; Sequence 1, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-1

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+07;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||||||||
Db      9 TTCNNNGAA 1


RESULT 3
US-08-411-020-10
; Sequence 10, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-10

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCCCGGAA 9


RESULT 4
US-08-411-020-10/c
; Sequence 10, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
```

```
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-10

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       9 TTCCGGGAA 1


RESULT 5
US-08-411-020-11
; Sequence 11, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-11

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       1 TTCCCCGAA 9


RESULT 6
US-08-411-020-11/c
; Sequence 11, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-11

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       9 TTCGGGGAA 1


RESULT 7
US-08-411-020-12
; Sequence 12, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-12

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCTAAGAA 9


RESULT 8
US-08-411-020-12/c
; Sequence 12, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-12

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCTTAGAA 1


RESULT 9
US-08-411-020-13
; Sequence 13, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-13

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCTCAGAA 9


RESULT 10
US-08-411-020-13/c
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; Sequence 13, Application US/08411020
; Patent No. 5712094
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    APPLICANT:  CHAN, SHIN-SHAY TIAN
;    TITLE OF INVENTION:  METHODS AND ASSOCIATED REAGENTS FOR
;    TITLE OF INVENTION:  DETECTING MODULATORS OF CYTOKINE ACTION
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ligand Pharmaceuticals Incorporated
;      STREET:  9393 Towne Centre Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/411,020
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jurgensen, Thomas E.
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0030.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-411-020-13

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db       9 TTCTGAGAA 1
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RESULT 11
US-08-369-796-25
; Sequence 25, Application US/08369796
; Patent No. 5716622
;  GENERAL INFORMATION:
;    APPLICANT:  James E. Darnell, Jr.
;    APPLICANT:  Zilong Wen
;    APPLICANT:  Curt M. Horvath
;    APPLICANT:  Zhong Zhong
;    TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;    TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/369,796
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-116
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA synthetic probe
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-369-796-25

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db       1 TTCCCGGAA 9
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```
RESULT 12
US-08-369-796-25/c
; Sequence 25, Application US/08369796
; Patent No. 5716622
;  GENERAL INFORMATION:
;    APPLICANT:  James E. Darnell, Jr.
;    APPLICANT:  Zilong Wen
;    APPLICANT:  Curt M. Horvath
;    APPLICANT:  Zhong Zhong
;    TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;    TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/369,796
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-116
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
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;       LENGTH:  9 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA synthetic probe
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-369-796-25

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       9 TTCCGGGAA 1


RESULT 13
US-08-369-796-26
; Sequence 26, Application US/08369796
; Patent No. 5716622
;  GENERAL INFORMATION:
;     APPLICANT:  James E. Darnell, Jr.
;     APPLICANT:  Zilong Wen
;     APPLICANT:  Curt M. Horvath
;     APPLICANT:  Zhong Zhong
;     TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;     TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;     NUMBER OF SEQUENCES:  39
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Klauber & Jackson
;       STREET:  411 Hackensack Avenue
;       CITY:  Hackensack
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07601
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/369,796
;       FILING DATE:  06-JAN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jackson Esq., David A.
;       REGISTRATION NUMBER:  26,742
;       REFERENCE/DOCKET NUMBER:  600-1-116
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201 487-5800
;       TELEFAX:  201 343-1684
;       TELEX:  133521
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  9 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA synthetic probe
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-369-796-26

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       1 TTCCGGGAA 9


RESULT 14
US-08-369-796-26/c
; Sequence 26, Application US/08369796
; Patent No. 5716622
;  GENERAL INFORMATION:
;     APPLICANT:  James E. Darnell, Jr.
;     APPLICANT:  Zilong Wen
;     APPLICANT:  Curt M. Horvath
;     APPLICANT:  Zhong Zhong
;     TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;     TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;     NUMBER OF SEQUENCES:  39
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Klauber & Jackson
;       STREET:  411 Hackensack Avenue
;       CITY:  Hackensack
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07601
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/369,796
;       FILING DATE:  06-JAN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jackson Esq., David A.
;       REGISTRATION NUMBER:  26,742
;       REFERENCE/DOCKET NUMBER:  600-1-116
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201 487-5800
;       TELEFAX:  201 343-1684
;       TELEX:  133521
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  9 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA synthetic probe
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-369-796-26

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       9 TTCCCGGAA 1


RESULT 15
US-08-369-796-27
; Sequence 27, Application US/08369796
; Patent No. 5716622
;  GENERAL INFORMATION:
;     APPLICANT:  James E. Darnell, Jr.
;     APPLICANT:  Zilong Wen
;     APPLICANT:  Curt M. Horvath
;     APPLICANT:  Zhong Zhong
;     TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;     TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;     NUMBER OF SEQUENCES:  39
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Klauber & Jackson
;       STREET:  411 Hackensack Avenue
;       CITY:  Hackensack
```

```
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07601
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/369,796
;       FILING DATE:  06-JAN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jackson Esq., David A.
;       REGISTRATION NUMBER:  26,742
;       REFERENCE/DOCKET NUMBER:  600-1-116
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201 487-5800
;       TELEFAX:  201 343-1684
;       TELEX:  133521
;   INFORMATION FOR SEQ ID NO:  27:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  9 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA synthetic probe
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-369-796-27

  Query Match             66.7%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       1 TTCCGGGAA 9


Search completed: December 25, 2002, 20:21:58
Job time : 53 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:24:48 ; Search time 227 Seconds
(without alignments)
28.371 Million cell updates/sec

Title: US-09-744-875-1
Perfect score: 21
Sequence: 1 agatttctaggaattcaaatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	85.7	21	1	US-08-366-276-8	Sequence 8, Appli
	2	18	85.7	100	4	US-09-522-217-59	Sequence 59, Appl
c	3	18	85.7	100	4	US-09-522-217-60	Sequence 60, Appl
	4	14.6	69.5	58	4	US-09-140-804-46	Sequence 46, Appl
	5	14.6	69.5	58	4	US-09-173-043-22	Sequence 22, Appl
	6	14.6	69.5	58	4	US-09-209-525-42	Sequence 42, Appl
c	7	14.2	67.6	20	4	US-09-662-402A-35	Sequence 35, Appl
c	8	13.8	65.7	30	1	US-08-201-697-12	Sequence 12, Appl
c	9	13.8	65.7	30	1	US-08-463-090B-24	Sequence 24, Appl
c	10	13.6	64.8	34	1	US-08-332-420-54	Sequence 54, Appl
	11	13.6	64.8	37	1	US-07-941-363-1	Sequence 1, Appli
c	12	13.6	64.8	38	4	US-09-143-634-28	Sequence 28, Appl
	13	13.6	64.8	40	1	US-08-308-196A-4	Sequence 4, Appli
	14	13.6	64.8	40	4	US-09-289-803-3	Sequence 3, Appli
	15	13.6	64.8	40	5	PCT-US91-06452-4	Sequence 4, Appli
	16	13.6	64.8	41	4	US-09-289-803-2	Sequence 2, Appli
	17	13.6	64.8	42	4	US-09-289-803-1	Sequence 1, Appli
	18	13.6	64.8	68	6	5221737-7	Patent No. 5221737
	19	13.4	63.8	30	3	US-09-030-613-30	Sequence 30, Appl
	20	13.4	63.8	30	4	US-09-451-905-30	Sequence 30, Appl
	21	13.4	63.8	40	4	US-09-313-221A-77	Sequence 77, Appl
c	22	13.2	62.9	25	3	US-08-840-316-5	Sequence 5, Appli
c	23	13.2	62.9	25	4	US-08-809-523-5	Sequence 5, Appli
c	24	13.2	62.9	25	4	US-08-471-971-5	Sequence 5, Appli
c	25	13.2	62.9	25	4	US-09-402-776-5	Sequence 5, Appli
c	26	13.2	62.9	25	5	PCT-US93-08849A-5	Sequence 5, Appli
c	27	13.2	62.9	25	5	PCT-US93-08849-5	Sequence 5, Appli
c	28	13.2	62.9	31	3	US-09-182-816-30	Sequence 30, Appl
c	29	13.2	62.9	31	3	US-09-471-528-30	Sequence 30, Appl
c	30	13.2	62.9	31	4	US-09-634-530-30	Sequence 30, Appl
c	31	13.2	62.9	33	1	US-07-955-041-6	Sequence 6, Appli
c	32	13.2	62.9	33	1	US-08-227-455-6	Sequence 6, Appli
c	33	13.2	62.9	33	1	US-08-472-482-6	Sequence 6, Appli
c	34	13.2	62.9	33	1	US-08-487-069-6	Sequence 6, Appli
c	35	13.2	62.9	33	4	US-08-169-715-47	Sequence 47, Appl
	36	13.2	62.9	63	4	US-09-140-804-38	Sequence 38, Appl
c	37	13.2	62.9	72	1	US-08-413-118-122	Sequence 122, App
c	38	13.2	62.9	72	3	US-08-473-446-122	Sequence 122, App
c	39	13	61.9	21	1	US-08-242-680-14	Sequence 14, Appl
c	40	13	61.9	21	2	US-08-653-382A-14	Sequence 14, Appl
	41	13	61.9	26	2	US-08-215-089-4	Sequence 4, Appli
	42	13	61.9	26	5	PCT-US95-03384-4	Sequence 4, Appli
c	43	13	61.9	27	1	US-08-480-604A-15	Sequence 15, Appl
c	44	13	61.9	27	2	US-08-405-496A-15	Sequence 15, Appl
c	45	13	61.9	27	4	US-08-915-136-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-366-276-8
; Sequence 8, Application US/08366276
; Patent No. 5534409
; GENERAL INFORMATION:
; APPLICANT: Groner, Bernd
; APPLICANT: Gouilleux, Fabrice
; APPLICANT: Wakao, Hiroshi
; TITLE OF INVENTION: Cytokine Regulated Transcription Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,276
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9409396.0
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scoot
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: 4-19992/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "MGF binding sequence from
; DESCRIPTION: bovine b-casein"
; HYPOTHETICAL: NO
US-08-366-276-8

Query Match 85.7%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db      1 AGATTTCTAGGAATTCAA 18
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claim 13, 17, 20 sequence

RESULT 2
US-09-522-217-59
; Sequence 59, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC12749
US-09-522-217-59

Query Match 85.7%; Score 18; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAA 84
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RESULT 3
US-09-522-217-60/c
; Sequence 60, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC12748
US-09-522-217-60

Query Match 85.7%; Score 18; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21
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RESULT 4
US-09-140-804-46
; Sequence 46, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC14819
US-09-140-804-46

Query Match 69.5%; Score 14.6; DB 4; Length 58;
Best Local Similarity 81.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 AGATTTCTAGGAATTCAAATC 21
          ||| | |||||||||| | ||
Db     14 AGAATACTAGGAATTCTATTC 34
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RESULT 5
US-09-173-043-22
; Sequence 22, Application US/09173043
; Patent No. 6207442
; GENERAL INFORMATION:
; APPLICANT: Raymond, Christopher K.
; TITLE OF INVENTION: PLASMID CONSTRUCTION BY HOMOLOGOUS
; TITLE OF INVENTION: RECOMBINATION
; FILE REFERENCE: 97-27
; CURRENT APPLICATION NUMBER: US/09/173,043
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: US 60/062,061
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence

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;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
US-09-173-043-22

  Query Match             69.5%;  Score 14.6;  DB 4;  Length 58;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAATC 21
          ||| | ||||||||||  | ||
Db     14 AGAATACTAGGAATTCTACTC 34


RESULT 6
US-09-209-525-42
; Sequence 42, Application US/09209525
; Patent No. 6303770
; GENERAL INFORMATION:
;  APPLICANT: Lok, Si
;  APPLICANT: Conklin, Darrell C.
;  APPLICANT: Parrish, Julia E.
;  TITLE OF INVENTION: Mammalian Alpha Helical Protein-1
;  FILE REFERENCE: 97-71
;  CURRENT APPLICATION NUMBER: US/09/209,525
;  CURRENT FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
;   LENGTH: 58
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-209-525-42

  Query Match             69.5%;  Score 14.6;  DB 4;  Length 58;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAATC 21
          ||| | ||||||||||  | ||
Db     14 AGAATACTAGGAATTCTACTC 34


RESULT 7
US-09-662-402A-35/c
; Sequence 35, Application US/09662402A
; Patent No. 6420117
; GENERAL INFORMATION:
;  APPLICANT: Wessler, Susan R
;  APPLICANT:  Casa, Alexandra M
;  TITLE OF INVENTION: MINIATURE INVERTED REPEAT TRANSPOSABLE ELEMENTS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 235.00230101
;  CURRENT APPLICATION NUMBER: US/09/662,402A
;  CURRENT FILING DATE:  2000-09-14
;  PRIOR APPLICATION NUMBER: 60/153,812
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide primer
US-09-662-402A-35

  Query Match             67.6%;  Score 14.2;  DB 4;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 ATTTCTAGGAATTCAAATC 21
          ||||| |||||||  ||||
Db     19 ATTTCGAGGAATTGGAATC 1


RESULT 8
US-08-201-697-12/c
; Sequence 12, Application US/08201697
; Patent No. 5705623
;  GENERAL INFORMATION:
;    APPLICANT:  Wiggins, Roger C.
;    APPLICANT:  Thomas, Peedikayil E.
;    TITLE OF INVENTION:  Mammalian Glomerular Epithelial Protein
;    TITLE OF INVENTION:  1
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/201,697
;      FILING DATE:  25-FEB-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryb A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UM 9783
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:. 12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-201-697-12

  Query Match             65.7%;  Score 13.8;  DB 1;  Length 30;
  Best Local Similarity   88.2%;  Pred. No. 6.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 ATTTCTAGGAATTCAAA 19
          | | ||||||||||||||
Db     17 AGTCCTAGGAATTCAAA 1


RESULT 9
US-08-463-090B-24/c
; Sequence 24, Application US/08463090B
; Patent No. 5801015
;  GENERAL INFORMATION:
;    APPLICANT:  Cottarel, Guillaume
;    APPLICANT:  Damagnez, Veronique
;    APPLICANT:  Draetta, Guilio
;    TITLE OF INVENTION:  Cell-Cycle Regulatory Proteins from
;    TITLE OF INVENTION:  Human Pathogens, and Uses Related Thereto
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot, LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,090B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV032.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1299
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
US-08-463-090B-24

  Query Match             65.7%;  Score 13.8;  DB 1;  Length 30;
  Best Local Similarity   88.2%;  Pred. No. 6.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 ATTTCTAGGAATTCAAA 19
           ||| ||| |||||||||
Db      20 ATTACTATGAATTCAAA 4


RESULT 10
US-08-332-420-54/c
; Sequence 54, Application US/08332420
; Patent No. 5744300
;  GENERAL INFORMATION:
;    APPLICANT:  Maarten H.K. Linskens, et al.
;    TITLE OF INVENTION:  METHODS AND REAGENTS FOR THE
;    TITLE OF INVENTION:  IDENTIFICATION AND REGULATION
;    TITLE OF INVENTION:  OF SENESCENCE-RELATED GENES
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,420
;      FILING DATE:  October 31, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/235,180
;      FILING DATE:  April 29, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/041
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-332-420-54

  Query Match             64.8%;  Score 13.6;  DB 1;  Length 34;
  Best Local Similarity   80.0%;  Pred. No. 7.8e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 AGATTTCTAGGAATTCAAAT 20
           |||  || | ||||||||||
Db      32 AGAGATCGAAGAATTCAAAT 13


RESULT 11
US-07-941-363-1
; Sequence 1, Application US/07941363
; Patent No. 5348886
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Stephen C.
;    APPLICANT:  Luckow, Verne A.
;    APPLICANT:  Leusch, Mark S.
;    APPLICANT:  Olins, Peter O.
;    TITLE OF INVENTION:  Method of Producing Recombinant
;    TITLE OF INVENTION:  Eukaryotic Viruses in Bacteria
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, Monsanto Co., A3SG
;      STREET:  800 N. Lindbergh Blvd.
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63167
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/941,363
;      FILING DATE:  19920904
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  07-21(872)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)694-5402
;      TELEFAX:  (314)694-9009
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-941-363-1

  Query Match             64.8%;  Score 13.6;  DB 1;  Length 37;
  Best Local Similarity   80.0%;  Pred. No. 7.8e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 AGATTTCTAGGAATTCAAAT 20
           |||| |  ||||||||| ||
Db       1 AGATCTGCAGGAATTCACAT 20


RESULT 12
US-09-143-634-28/c
; Sequence 28, Application US/09143634
; Patent No. 6214602
; GENERAL INFORMATION:
;  APPLICANT: Zdanovsky, Alexey G.
;  TITLE OF INVENTION: EXPRESSION OF CLOSTRIDIAL TOXINS AND PROTEINS
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;  FILE REFERENCE: PRMG-03193
;  CURRENT APPLICATION NUMBER: US/09/143,634
;  CURRENT FILING DATE: 1998-08-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 38
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-143-634-28

  Query Match            64.8%;  Score 13.6;  DB 4;  Length 38;
  Best Local Similarity   80.0%;  Pred. No. 7.8e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 GATTTCTAGGAATTCAAATC 21
          ||| | || ||||||| |||
Db     21 GATATTTAAGAATTCAGATC 2


RESULT 13
US-08-308-196A-4
; Sequence 4, Application US/08308196A
; Patent No. 5612198
;  GENERAL INFORMATION:
;    APPLICANT:  Brierley, Russell A.
;    APPLICANT:  Davis, Geneva R.
;    APPLICANT:  Holtz, Gregory C.
;    APPLICANT:  Gleeson, Martin A.
;    APPLICANT:  Howard, Bradley D.
;    TITLE OF INVENTION:  Production of Insulin-Like Growth
;    TITLE OF INVENTION:  Factor-1 in Methylotrophic Yeast Cells
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/308,196A
;      FILING DATE:  09-SEPT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/983,523
;      FILING DATE:  03-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/578,728
;      FILING DATE:  04-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  51875
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic DNA)
US-08-308-196A-4

  Query Match            64.8%;  Score 13.6;  DB 1;  Length 40;
  Best Local Similarity   80.0%;  Pred. No. 7.9e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAAT 20
          || ||  || ||||||||||
Db      5 AGCTTGATAAGAATTCAAAT 24


RESULT 14
US-09-289-803-3
; Sequence 3, Application US/09289803
; Patent No. 6162605
; GENERAL INFORMATION:
;  APPLICANT: Fort, Thomas L.
;  APPLICANT: McMillian, Ray A.
;  APPLICANT: Hellyer, Tobin
;  APPLICANT: You, Qimin
;  TITLE OF INVENTION: Amplification and Detection of Shiga-Like Toxin I
;  TITLE OF INVENTION: Producing Organsims
;  FILE REFERENCE: SLT-I Application
;  CURRENT APPLICATION NUMBER: US/09/289,803
;  CURRENT FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer for SDA
;   OTHER INFORMATION: of SLT-I Producing Organisms
US-09-289-803-3

  Query Match            64.8%;  Score 13.6;  DB 4;  Length 40;
  Best Local Similarity   80.0%;  Pred. No. 7.9e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAAT 20
          ||| |||| || ||||| ||
Db     13 AGACTTCTCGGGATTCACAT 32


RESULT 15
PCT-US91-06452-4
; Sequence 4, Application PC/TUS9106452
;  GENERAL INFORMATION:
;    APPLICANT:  Brierley, Russell A.
;    APPLICANT:  Davis, Geneva R.
;    APPLICANT:  Holtz, Gregory C.
;    APPLICANT:  Gleeson, Martin A.
;    APPLICANT:  Bradley, D. H.
;    TITLE OF INVENTION:  Production of Insulin-Like Growth
;    TITLE OF INVENTION:  Factor-1 in Methylotrophic Yeast Cells
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 South LaSalle Street, Suite 900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/06452
;      FILING DATE:  19910409
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/578,728
;      FILING DATE:  04-SEP-1990
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  51874
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)552-1311
;      TELEFAX:  (619)552-0095
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
PCT-US91-06452-4

  Query Match             64.8%;  Score 13.6;  DB 5;  Length 40;
  Best Local Similarity   80.0%;  Pred. No. 7.9e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 AGATTTCTAGGAATTCAAAT 20
           || ||  || ||||||||||
Db       5 AGCTTGATAAGAATTCAAAT 24


Search completed: December 25, 2002, 11:36:14
Job time : 229 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:24:49 ; Search time 262 Seconds
(without alignments)
77.359 Million cell updates/sec

Title: SCHMIDT875
Perfect score: 9
Sequence: 1 ttcnnngaa 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	66.7	9	16	AAT14120	Cytokine responsiv
c	2	6	66.7	9	16	AAT14120	Cytokine responsiv
	3	6	66.7	9	16	AAT14165	Cytokine responsiv
c	4	6	66.7	9	16	AAT14165	Cytokine responsiv
	5	6	66.7	9	16	AAT14149	Cytokine responsiv
c	6	6	66.7	9	16	AAT14149	Cytokine responsiv
	7	6	66.7	9	16	AAT14145	Cytokine responsiv
c	8	6	66.7	9	16	AAT14145	Cytokine responsiv
	9	6	66.7	9	16	AAT14147	Cytokine responsiv
c	10	6	66.7	9	16	AAT14147	Cytokine responsiv
	11	6	66.7	9	16	AAT14140	Cytokine responsiv
c	12	6	66.7	9	16	AAT14140	Cytokine responsiv
	13	6	66.7	9	16	AAT14142	Cytokine responsiv
c	14	6	66.7	9	16	AAT14142	Cytokine responsiv
	15	6	66.7	9	16	AAT14137	Cytokine responsiv
c	16	6	66.7	9	16	AAT14137	Cytokine responsiv
	17	6	66.7	9	17	AAT41581	Cytokine activated
c	18	6	66.7	9	17	AAT41581	Cytokine activated
	19	6	66.7	9	17	AAT41580	Cytokine activated
c	20	6	66.7	9	17	AAT41580	Cytokine activated
	21	6	66.7	9	17	AAT41582	Cytokine activated
c	22	6	66.7	9	17	AAT41582	Cytokine activated
	23	6	66.7	9	17	AAT41583	Cytokine activated
c	24	6	66.7	9	17	AAT41583	Cytokine activated
	25	6	66.7	9	19	AAV56892	Regulatory element
c	26	6	66.7	9	19	AAV56892	Regulatory element
	27	6	66.7	9	19	AAV56876	Regulatory element
c	28	6	66.7	9	19	AAV56876	Regulatory element
	29	6	66.7	9	19	AAV56864	Regulatory element
c	30	6	66.7	9	19	AAV56864	Regulatory element
	31	6	66.7	9	19	AAV56867	Regulatory element
c	32	6	66.7	9	19	AAV56867	Regulatory element
	33	6	66.7	9	19	AAV56869	Regulatory element
c	34	6	66.7	9	19	AAV56869	Regulatory element
	35	6	66.7	9	19	AAV56872	Regulatory element
c	36	6	66.7	9	19	AAV56872	Regulatory element
	37	6	66.7	9	19	AAV56874	Regulatory element
c	38	6	66.7	9	19	AAV56874	Regulatory element
	39	6	66.7	9	19	AAV56847	Regulatory element
c	40	6	66.7	9	19	AAV56847	Regulatory element
	41	6	66.7	9	19	AAV11639	Fc-gamma RI promot
c	42	6	66.7	9	19	AAV11639	Fc-gamma RI promot
	43	6	66.7	9	21	AAC83341	Interleukin-6 resp
c	44	6	66.7	9	21	AAC83341	Interleukin-6 resp
	45	6	66.7	9	21	AAA61935	STAT response elem

ALIGNMENTS

RESULT 1
AAT14120
ID AAT14120 standard; DNA; 9 BP.
XX
AC AAT14120;
XX
DT 30-MAY-1996 (first entry)
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
KW Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS Synthetic.
XX
PN WO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US04477.
XX
PR 27-MAR-1995; 95US-0410780.
PR 14-APR-1994; 94US-0228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb IP, Seidel HM;
XX
DR WPI; 1995-373797/48.
XX
PT DNA spacer regulatory elements responsive to cytokine(s) - for

PT detecting the presence of transcriptional regulatory protein in a
PT sample
XX
PS Disclosure; Page 18; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element
CC TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC activated transcriptional regulatory protein in response to a
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC spacer regulatory element can be used to detect the presence of
CC a transcriptional regulatory protein in a sample, and in assays
CC for (ant)agonists of gene transcription. The identified cpds.
CC may be used to treat cytokine-induced disease states, or to
CC ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ Sequence 9 BP; 2 A; 1 C; 1 G; 2 T; 3 other;

Query Match 66.7%; Score 6; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCNNNGAA 9
|||||||||
Db 1 TTCNNNGAA 9

RESULT 2
AAT14120/c
ID AAT14120 standard; DNA; 9 BP.
XX
AC AAT14120;
XX
DT 30-MAY-1996 (first entry)
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
KW Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS Synthetic.
XX
PN WO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US04477.
XX
PR 27-MAR-1995; 95US-0410780.
PR 14-APR-1994; 94US-0228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb IP, Seidel HM;
XX
DR WPI; 1995-373797/48.
XX
PT DNA spacer regulatory elements responsive to cytokine(s) - for
PT detecting the presence of transcriptional regulatory protein in a
PT sample
XX
PS Disclosure; Page 18; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element
CC TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC activated transcriptional regulatory protein in response to a
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC spacer regulatory element can be used to detect the presence of
CC a transcriptional regulatory protein in a sample, and in assays
CC for (ant)agonists of gene transcription. The identified cpds.
CC may be used to treat cytokine-induced disease states, or to
CC ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ Sequence 9 BP; 2 A; 1 C; 1 G; 2 T; 3 other;

Query Match 66.7%; Score 6; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCNNNGAA 9
|||||||||
Db 9 TTCNNNGAA 1

RESULT 3
AAT14165
ID AAT14165 standard; DNA; 9 BP.
XX
AC AAT14165;
XX
DT 29-MAY-1996 (first entry)
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
KW Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS Synthetic.
XX
PN WO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US04477.
XX
PR 27-MAR-1995; 95US-0410780.
PR 14-APR-1994; 94US-0228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb IP, Seidel HM;
XX
DR WPI; 1995-373797/48.
XX
PT DNA spacer regulatory elements responsive to cytokine(s) - for
PT detecting the presence of transcriptional regulatory protein in a
PT sample
XX
PS Claim 7; Page 125; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element
CC TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC activated transcriptional regulatory protein in response to a
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC spacer regulatory element can be used to detect the presence of
CC a transcriptional regulatory protein in a sample, and in assays
CC for (ant)agonists of gene transcription. The identified cpds.
CC may be used to treat cytokine-induced disease states, or to
CC ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match 66.7%; Score 6; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.4e+08;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTCNNNGAA 9
||| |||
Db 1 TTCTAAGAA 9

RESULT 4

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AAT14165/c
ID   AAT14165 standard; DNA; 9 BP.
XX
AC   AAT14165;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db       9 TTCTTAGAA 1


RESULT 5
AAT14149
ID   AAT14149 standard; DNA; 9 BP.
XX
AC   AAT14149;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db       1 TTCTCAGAA 9


RESULT 6
AAT14149/c
ID   AAT14149 standard; DNA; 9 BP.
XX
AC   AAT14149;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
```

```
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCTGAGAA 1


RESULT 7
AAT14145
ID   AAT14145 standard; DNA; 9 BP.
XX
AC   AAT14145;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 3 A; 3 C; 1 G; 2 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCCCAGAA 9


RESULT 8
AAT14145/c
ID   AAT14145 standard; DNA; 9 BP.
XX
AC   AAT14145;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 3 A; 3 C; 1 G; 2 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCTGGGAA 1
```

```
RESULT 9
AAT14147
ID   AAT14147 standard; DNA; 9 BP.
XX
AC   AAT14147;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 1 G; 5 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCTTTGAA 9


RESULT 10
AAT14147/c
ID   AAT14147 standard; DNA; 9 BP.
XX
AC   AAT14147;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 1 G; 5 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCAAAGAA 1


RESULT 11
AAT14140
ID   AAT14140 standard; DNA; 9 BP.
XX
AC   AAT14140;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
```

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XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 2 A; 3 C; 2 G; 2 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCCCGGAA 9


RESULT 12
AAT14140/c
ID   AAT14140 standard; DNA; 9 BP.
XX
AC   AAT14140;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 2 A; 3 C; 2 G; 2 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCCGGGAA 1


RESULT 13
AAT14142
ID   AAT14142 standard; DNA; 9 BP.
XX
AC   AAT14142;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 2 A; 2 C; 2 G; 3 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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```
Qy      1 TTCNNNGAA 9
            |||   |||
Db      1 TTCCTGGAA 9


RESULT 14
AAT14142/c
ID   AAT14142 standard; DNA; 9 BP.
XX
AC   AAT14142;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 2 A; 2 C; 2 G; 3 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
            |||   |||
Db      9 TTCCAGGAA 1


RESULT 15
AAT14137
ID   AAT14137 standard; DNA; 9 BP.
XX
AC   AAT14137;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;   95WO-US04477.
XX
PR   27-MAR-1995;   95US-0410780.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 124; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 2 A; 4 C; 1 G; 2 T; 0 other;

  Query Match             66.7%;  Score 6;  DB 16;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+08;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
            |||   |||
Db      1 TTCCCCGAA 9


Search completed: December 25, 2002, 18:15:59
Job time : 263 secs
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:24:48 ; Search time 242 Seconds
(without alignments)
35.252 Million cell updates/sec

Title: US-09-744-875-1
Perfect score: 21
Sequence: 1 agatttctaggaattcaaatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 221248

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	85.7	100	10	US-09-923-246-59	Sequence 59, Appl
c	2	18	85.7	100	10	US-09-923-246-60	Sequence 60, Appl
	3	18	85.7	100	10	US-09-825-561A-48	Sequence 48, Appl
c	4	18	85.7	100	10	US-09-825-561A-49	Sequence 49, Appl
	5	14.6	69.5	58	10	US-09-932-679-42	Sequence 42, Appl
c	6	14.2	67.6	99	10	US-09-969-373-1158	Sequence 1158, Ap
	7	13	61.9	22	9	US-09-881-012-130	Sequence 130, App
c	8	13	61.9	30	10	US-09-927-933A-14	Sequence 14, Appl
	9	13	61.9	30	10	US-09-927-933A-15	Sequence 15, Appl
c	10	13	61.9	50	9	US-09-832-659-10	Sequence 10, Appl
c	11	13	61.9	50	9	US-09-832-659-30	Sequence 30, Appl
	12	12.8	61.0	30	10	US-09-792-420-11	Sequence 11, Appl
c	13	12.8	61.0	33	10	US-09-863-179-2	Sequence 2, Appli
c	14	12.8	61.0	98	10	US-09-878-574-3000	Sequence 3000, Ap
c	15	12.6	60.0	37	9	US-09-843-905A-10	Sequence 10, Appl
	16	12.6	60.0	78	10	US-09-864-761-29850	Sequence 29850, A
	17	12.6	60.0	80	10	US-09-157-748-43	Sequence 43, Appl
	18	12.6	60.0	98	10	US-09-878-574-15211	Sequence 15211, A
	19	12.4	59.0	20	9	US-09-813-824A-25	Sequence 25, Appl
c	20	12.4	59.0	20	9	US-09-813-824A-25	Sequence 25, Appl
	21	12.4	59.0	28	10	US-09-921-068-4	Sequence 4, Appli
c	22	12.4	59.0	30	10	US-09-475-674-18	Sequence 18, Appl
c	23	12.4	59.0	37	10	US-09-737-178-140	Sequence 140, App
	24	12.4	59.0	74	10	US-09-783-590-2523	Sequence 2523, Ap
	25	12.2	58.1	24	9	US-09-992-598-190	Sequence 190, App
	26	12.2	58.1	24	9	US-09-989-293A-190	Sequence 190, App
	27	12.2	58.1	24	9	US-09-989-735-190	Sequence 190, App
	28	12.2	58.1	24	9	US-09-990-444-190	Sequence 190, App
	29	12.2	58.1	24	10	US-09-989-722-190	Sequence 190, App
	30	12.2	58.1	24	10	US-09-989-723-190	Sequence 190, App
	31	12.2	58.1	24	10	US-09-989-279-190	Sequence 190, App
	32	12.2	58.1	24	10	US-09-989-727-190	Sequence 190, App
	33	12.2	58.1	24	10	US-09-989-731-190	Sequence 190, App
	34	12.2	58.1	24	10	US-09-989-732-190	Sequence 190, App
	35	12.2	58.1	24	10	US-09-991-073-190	Sequence 190, App
	36	12.2	58.1	24	10	US-09-990-442-190	Sequence 190, App
	37	12.2	58.1	24	10	US-09-991-163-190	Sequence 190, App
	38	12.2	58.1	24	10	US-09-993-604-190	Sequence 190, App
	39	12.2	58.1	24	10	US-09-990-456-190	Sequence 190, App
	40	12.2	58.1	24	10	US-09-989-721-190	Sequence 190, App
	41	12.2	58.1	24	12	US-10-076-900-14	Sequence 14, Appl
c	42	12.2	58.1	26	9	US-09-887-593-17	Sequence 17, Appl
c	43	12.2	58.1	30	9	US-10-104-019-99	Sequence 99, Appl
	44	12.2	58.1	52	10	US-09-777-564-1717	Sequence 1717, Ap
c	45	12.2	58.1	60	9	US-10-006-611-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT 1
US-09-923-246-59
; Sequence 59, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
;  APPLICANT: No. US20020128446Alak, Julia E.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Holly, Richard D.
;  APPLICANT:  Gross, Jane A.
;  APPLICANT:  Johnston, Janet V.
;  APPLICANT:  Nelson, Andrew J.
;  APPLICANT:  Dillon, Stacey R.
;  APPLICANT:  Hammond, Angela K.
;  TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;  FILE REFERENCE: 99-16
;  CURRENT APPLICATION NUMBER: US/09/923,246
;  CURRENT FILING DATE:  2001-08-03
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
;  PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
;   LENGTH: 100
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide ZC12749
US-09-923-246-59

  Query Match             85.7%;  Score 18;  DB 10;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAA 84
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RESULT 2
US-09-923-246-60/c
; Sequence 60, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
;  APPLICANT: No. US20020128446A1ak, Julia E.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Holly, Richard D.
;  APPLICANT:  Gross, Jane A.
;  APPLICANT:  Johnston, Janet V.
;  APPLICANT:  Nelson, Andrew J.
;  APPLICANT:  Dillon, Stacey R.
;  APPLICANT:  Hammond, Angela K.
;  TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;  FILE REFERENCE: 99-16
;  CURRENT APPLICATION NUMBER: US/09/923,246
;  CURRENT FILING DATE:  2001-08-03
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
;  PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 60
;   LENGTH: 100
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide ZC12748
US-09-923-246-60

  Query Match             85.7%;  Score 18;  DB 10;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 3
US-09-825-561A-48
; Sequence 48, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT:  No. US20020137677A1ak, Julia E.
;  APPLICANT:  West, James W.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Holly, Richard D.
;  APPLICANT:  Nelson, Andrew J.
;  TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
;  FILE REFERENCE: 00-22
;  CURRENT APPLICATION NUMBER: US/09/825,561A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/194,731
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/222,121
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
;   LENGTH: 100
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer ZC12749
US-09-825-561A-48

  Query Match             85.7%;  Score 18;  DB 10;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     67 AGATTTCTAGGAATTCAA 84


RESULT 4
US-09-825-561A-49/c
; Sequence 49, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT:  No. US20020137677A1ak, Julia E.
;  APPLICANT:  West, James W.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Holly, Richard D.
;  APPLICANT:  Nelson, Andrew J.
;  TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
;  FILE REFERENCE: 00-22
;  CURRENT APPLICATION NUMBER: US/09/825,561A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/194,731
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/222,121
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49
;   LENGTH: 100
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer ZC12748
US-09-825-561A-49

  Query Match             85.7%;  Score 18;  DB 10;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAA 18
          ||||||||||||||||||
Db     38 AGATTTCTAGGAATTCAA 21


RESULT 5
US-09-932-679-42
; Sequence 42, Application US/09932679
; Patent No. US20020058801A1
; GENERAL INFORMATION:
;  APPLICANT: Lok, Si
;  APPLICANT:  Conklin, Darrell C.
;  APPLICANT:  No. US20020058801A1ak, Julia E.
;  TITLE OF INVENTION: Mammalian Alpha Helical Protein-1
;  FILE REFERENCE: 97-71D1
;  CURRENT APPLICATION NUMBER: US/09/932,679
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: 09/209,525
;  PRIOR FILING DATE: 1998-12-10
;  PRIOR APPLICATION NUMBER: 60/067,779
;  PRIOR FILING DATE: 1997-12-10
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;   LENGTH: 58
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-932-679-42
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  Query Match            69.5%;  Score 14.6;  DB 10;  Length 58;
  Best Local Similarity  81.0%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAATC 21
          ||| | |||||||||| | ||
Db     14 AGAATACTAGGAATTCTACTC 34


RESULT 6
US-09-969-373-1158/c
; Sequence 1158, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
;  APPLICANT: Effertz, Roger J.
;  APPLICANT:  Hauge, Brian M.
;  TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;  FILE REFERENCE: 38-10(52679)A
;  CURRENT APPLICATION NUMBER: US/09/969,373
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 09/754,853
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 09/760,427
;  PRIOR FILING DATE: 2001-01-13
;  PRIOR APPLICATION NUMBER: US 09/855,768
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1158
;   LENGTH: 99
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-969-373-1158

  Query Match            67.6%;  Score 14.2;  DB 10;  Length 99;
  Best Local Similarity  84.2%;  Pred. No. 8.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 ATTTCTAGGAATTCAAATC 21
          |||| || ||||| |||||
Db     60 ATTTATATGAATTGAAATC 42


RESULT 7
US-09-881-012-130
; Sequence 130, Application US/09881012
; Publication No. US20020192655A1
; GENERAL INFORMATION:
;  APPLICANT: Ginns, Edward I.
;  APPLICANT:  Egeland, Janice A.
;  APPLICANT:  Paul, Steven M.
;  APPLICANT:  The Governmwent of the United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Susceptibility and Resistance Genes for
;  TITLE OF INVENTION:  Bipolar Affective Disorder
;  FILE REFERENCE: 015280-248110US
;  CURRENT APPLICATION NUMBER: US/09/881,012
;  CURRENT FILING DATE:  2001-06-13
;  PRIOR APPLICATION NUMBER: US/09/175,158
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: US 60/062,924
;  PRIOR FILING DATE: 1997-10-20
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 130
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: D4S1564 reverse primer
US-09-881-012-130

  Query Match            61.9%;  Score 13;  DB 9;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 2.5e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAA 13
          |||||||||||||
Db      2 AGATTTCTAGGAA 14


RESULT 8
US-09-927-933A-14/c
; Sequence 14, Application US/09927933A
; Patent No. US20020107869A1
; GENERAL INFORMATION:
;  APPLICANT: LEROY, Pierre
;  TITLE OF INVENTION: NOVEL IMPLANT AND NOVEL VECTOR FOR THE TREATMENT OF
;  TITLE OF INVENTION:  ACQUIRED DISEASES
;  FILE REFERENCE: 032751-012
;  CURRENT APPLICATION NUMBER: US/09/927,933A
;  CURRENT FILING DATE:  2001-08-13
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/809,110
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 94 10911
;  PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-13
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: human CD4 cDNA
US-09-927-933A-14

  Query Match            61.9%;  Score 13;  DB 10;  Length 30;
  Best Local Similarity  76.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAATC 21
          || |||| ||||   ||||||
Db     25 AGCTTTCCAGGAGCCCAAATC 5


RESULT 9
US-09-927-933A-15
; Sequence 15, Application US/09927933A
; Patent No. US20020107869A1
; GENERAL INFORMATION:
;  APPLICANT: LEROY, Pierre
;  TITLE OF INVENTION: NOVEL IMPLANT AND NOVEL VECTOR FOR THE TREATMENT OF
;  TITLE OF INVENTION:  ACQUIRED DISEASES
;  FILE REFERENCE: 032751-012
;  CURRENT APPLICATION NUMBER: US/09/927,933A
;  CURRENT FILING DATE:  2001-08-13
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/809,110
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 94 10911
;  PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-13
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: cDNA of heavy chain of antibody 2F5
US-09-927-933A-15

  Query Match            61.9%;  Score 13;  DB 10;  Length 30;
  Best Local Similarity  76.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAATC 21
          || |||| ||||   ||||||
Db      6 AGCTTTCCAGGAGCCCAAATC 26


RESULT 10
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US-09-832-659-10/c
; Sequence 10, Application US/09832659
; Patent No. US20020155547A1
; GENERAL INFORMATION:
;  APPLICANT: BIOGEN, INC.
;  TITLE OF INVENTION: Interferon-Beta Fusion Proteins and Uses
;  FILE REFERENCE: A064PCTSEQ
;  CURRENT APPLICATION NUMBER: US/09/832,659
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 60/120,237
;  PRIOR FILING DATE: 1999-02-16
;  PRIOR APPLICATION NUMBER: 60/104,491
;  PRIOR FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-832-659-10

  Query Match             61.9%;  Score 13;  DB 9;  Length 50;
  Best Local Similarity   76.2%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAATC 21
          || || |||||| ||||  ||
Db     26 AGTTTGCTAGGATTTCAGCTC 6


RESULT 11
US-09-832-659-30/c
; Sequence 30, Application US/09832659
; Patent No. US20020155547A1
; GENERAL INFORMATION:
;  APPLICANT: BIOGEN, INC.
;  TITLE OF INVENTION: Interferon-Beta Fusion Proteins and Uses
;  FILE REFERENCE: A064PCTSEQ
;  CURRENT APPLICATION NUMBER: US/09/832,659
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 60/120,237
;  PRIOR FILING DATE: 1999-02-16
;  PRIOR APPLICATION NUMBER: 60/104,491
;  PRIOR FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-832-659-30

  Query Match             61.9%;  Score 13;  DB 9;  Length 50;
  Best Local Similarity   76.2%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTCAAATC 21
          || || |||||| ||||  ||
Db     26 AGTTTGCTAGGATTTCAGCTC 6


RESULT 12
US-09-792-420-11
; Sequence 11, Application US/09792420
; Patent No. US20020055138A1
; GENERAL INFORMATION:
;  APPLICANT: Chien, Yueh-tyng
;  APPLICANT:  Thresher, Jason
;  APPLICANT:  Wobbe, C. Richard
;  APPLICANT:  Healy, Judith
;  TITLE OF INVENTION: STAPHYLOCOCCAL GTPase obg NUCLEOTIDE SEQUENCE ENCODING STAPHYLOCC
;  TITLE OF INVENTION:  GTP-BINDING PROTEIN
;  FILE REFERENCE: DN 1711 US
;  CURRENT APPLICATION NUMBER: US/09/792,420
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/184,742
;  PRIOR FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-09-792-420-11

  Query Match             61.0%;  Score 12.8;  DB 10;  Length 30;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      5 TTCTAGGAATTCAAAT 20
          ||| | ||||||||||
Db     13 TTCAACGAATTCAAAT 28


RESULT 13
US-09-863-179-2/c
; Sequence 2, Application US/09863179
; Patent No. US20020091094A1
; GENERAL INFORMATION:
;  APPLICANT: DURING, MATTHEW      KAPLITT, MICHAEL
;  TITLE OF INVENTION: GLUTAMIC ACID DECARBOXYLASE (GAD) BASED DELIVERY SYSTEM
;  FILE REFERENCE: 102182-12
;  CURRENT APPLICATION NUMBER: US/09/863,179
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: 60/206,281
;  PRIOR FILING DATE: 2000-05-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-863-179-2

  Query Match             61.0%;  Score 12.8;  DB 10;  Length 33;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 AGATTTCTAGGAATTC 16
          |||||| || ||||||
Db     22 AGATTTATAAGAATTC 7


RESULT 14
US-09-878-574-3000/c
; Sequence 3000, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT:  La Rosa, Thomas J.
;  APPLICANT:  Thompson, Michael D.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(15401)B
;  CURRENT APPLICATION NUMBER: US/09/878,574
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 09/333,535
;  PRIOR FILING DATE: 1999-06-14
;  NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3000
;   LENGTH: 98
;   TYPE: DNA
;   ORGANISM: Glycine max
;   OTHER INFORMATION: Clone ID: LIB3028-017-Q1-B1-D5
US-09-878-574-3000
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Query Match 61.0%; Score 12.8; DB 10; Length 98;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       5 TTCTAGGAATTCAAAT 20
           || |||||||||| |
Db      64 TTATAGGAATTCAATT 49
```

RESULT 15
US-09-843-905A-10/c
; Sequence 10, Application US/09843905A
; Patent No. US20020168683A1
; GENERAL INFORMATION:
; APPLICANT: Bird, Timothy A.
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES
; FILE REFERENCE: 2990-A
; CURRENT APPLICATION NUMBER: US/09/843,905A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,198
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-09-843-905A-10

Query Match 60.0%; Score 12.6; DB 9; Length 37;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2 GATTTCTAGGAATTCAAAT 20
           |||   |||||||||| ||
Db      24 GATAAGTAGGAATTCATAT 6
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Search completed: December 25, 2002, 11:40:36
Job time : 243 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 11:24:49 ; Search time 2979 Seconds
(without alignments)
114.168 Million cell updates/sec

Title: US-09-744-875-1
Perfect score: 21
Sequence: 1 agatttctaggaattcaaatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16.2	77.1	82	9	AI218421	AI218421 qh24b10.x
	2	15.2	72.4	84	17	AZ782789	AZ782789 2M0023P07
	3	14.6	69.5	73	9	AA749115	AA749115 oa58g04.s
c	4	14.4	68.6	63	10	AW695026	AW695026 NF082E06S
	5	14.4	68.6	97	17	AZ437380	AZ437380 1M0225B12
	6	14.2	67.6	48	17	BH851999	BH851999 SALK_0740
c	7	14.2	67.6	60	12	BG153679	BG153679 nag58g08.
	8	14.2	67.6	83	9	AI966296	AI966296 sc36h04.y
c	9	13.8	65.7	47	13	BJ077154	BJ077154 BJ077154
	10	13.8	65.7	49	9	AA422541	AA422541 vf14c03.s
c	11	13.8	65.7	69	17	AZ810918	AZ810918 2M0076K14
c	12	13.8	65.7	69	17	AZ956832	AZ956832 2M0223C05
c	13	13.8	65.7	76	12	BG153467	BG153467 nag49a01.
c	14	13.8	65.7	82	12	BG151684	BG151684 nag63b11.
c	15	13.8	65.7	88	12	BG151856	BG151856 nag65d05.
	16	13.8	65.7	91	17	AF087391	AF087391 AF087391
	17	13.8	65.7	91	17	BH758017	BH758017 SALK_0130
	18	13.6	64.8	48	17	BH615007	BH615007 BG00015-3
	19	13.6	64.8	50	12	BF789276	BF789276 602105183
c	20	13.6	64.8	63	12	BF463652	BF463652 UI-M-CG0p
c	21	13.6	64.8	71	12	BG668331	BG668331 DRACQH10
	22	13.6	64.8	86	9	AA863156	AA863156 og91c09.s
c	23	13.6	64.8	92	14	D75616	D75616 CELK107D2F
	24	13.6	64.8	94	17	BH218165	BH218165 1006077E0
	25	13.6	64.8	96	13	BM181183	BM181183 fw20c09.y
	26	13.6	64.8	96	17	CNS00UHH	AL090995 Arabidops
	27	13.4	63.8	88	14	N73593	N73593 za51c01.s1
	28	13.4	63.8	100	9	AA420566	AA420566 nc61b02.r
c	29	13.2	62.9	52	10	AW697073	AW697073 NF112A08S
	30	13.2	62.9	61	17	BH218412	BH218412 1006078F1
c	31	13.2	62.9	72	14	BQ754476	BQ754476 EBed01_SQ
	32	13.2	62.9	76	9	AU011284	AU011284 AU011284
c	33	13.2	62.9	78	17	AZ774680	AZ774680 2M0004P12
c	34	13.2	62.9	78	17	BH854811	BH854811 SALK_0884
c	35	13.2	62.9	78	17	BH854812	BH854812 SALK_0884
c	36	13.2	62.9	79	9	AI916764	AI916764 wc25c04.x
c	37	13.2	62.9	89	10	AW712808	AW712808 g3f11ne.r
	38	13.2	62.9	90	17	BH218396	BH218396 1006078F0
	39	13.2	62.9	92	9	AU259036	AU259036 AU259036
	40	13.2	62.9	92	10	BE575638	BE575638 dc60g08.x
	41	13.2	62.9	93	9	AA877878	AA877878 nr07b08.s
c	42	13.2	62.9	94	10	AW518820	AW518820 ha43f03.x
	43	13.2	62.9	96	17	BH251012	BH251012 SALK_0108
c	44	13.2	62.9	97	13	BI942693	BI942693 sk57a02.y
c	45	13.2	62.9	100	17	BH170159	BH170159 SALK_0024

ALIGNMENTS

RESULT 1
AI218421
LOCUS AI218421 82 bp mRNA linear EST 30-NOV-1998
DEFINITION qh24b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845595 3', mRNA sequence.
ACCESSION AI218421
VERSION AI218421.1 GI:3798236
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 82)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 925 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 73.
FEATURES Location/Qualifiers
source 1. .82
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1845595"

/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 37 a 11 c 13 g 21 t
ORIGIN

Query Match 77.1%; Score 16.2; DB 9; Length 82;
Best Local Similarity 85.7%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAAATC 21
| ||||||||||||| ||| |
Db 46 AAATTTCTAGGAATTAAAAGC 66

RESULT 2
AZ782789
LOCUS AZ782789 84 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0023P07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0023P07 R, DNA sequence.
ACCESSION AZ782789
VERSION AZ782789.1 GI:12916863
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 84)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0023 row: P column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 84.
FEATURES Location/Qualifiers
source 1. .84
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0023P07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 24 a 18 c 14 g 28 t
ORIGIN

Query Match 72.4%; Score 15.2; DB 17; Length 84;
Best Local Similarity 85.0%; Pred. No. 8.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAAAT 20
|| ||||||| |||||| ||
Db 23 AGTTTTCTAGTAATTCAGAT 42

RESULT 3
AA749115
LOCUS AA749115 73 bp mRNA linear EST 27-JAN-1998
DEFINITION oa58g04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309206 3', mRNA sequence.
ACCESSION AA749115
VERSION AA749115.1 GI:2789073
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 73)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 805 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 65.
FEATURES Location/Qualifiers
source 1. .73
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1309206"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3'

]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 29 a 10 c 7 g 27 t
ORIGIN

Query Match 69.5%; Score 14.6; DB 9; Length 73;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 AGATTTCTAGGAATTCAAATC 21
           ||||||| ||||| |  ||||
Db      17 AGATTTCAAGGAAATTTAATC 37
```

RESULT 4
AW695026/c
LOCUS AW695026 63 bp mRNA linear EST 21-DEC-2000
DEFINITION NF082E06ST1F1050 Developing stem Medicago truncatula cDNA clone NF082E06ST 5', mRNA sequence.
ACCESSION AW695026
VERSION AW695026.2 GI:11957373
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 63)
AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library
JOURNAL Unpublished (2000)
COMMENT On Apr 14, 2000 this sequence version replaced gi:7569788.
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 685 Std Error: 0.00
Plate: 082 row: E column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
source 1. .63
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF082E06ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
BASE COUNT 31 a 16 c 5 g 11 t
ORIGIN

Query Match 68.6%; Score 14.4; DB 10; Length 63;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       5 TTCTAGGAATTCAAAT 20
           || ||||||||||||||
Db      30 TTGTAGGAATTCAAAT 15
```

RESULT 5
AZ437380
LOCUS AZ437380 97 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0225B12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0225B12 R, DNA sequence.
ACCESSION AZ437380
VERSION AZ437380.1 GI:10561393
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 97)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: B column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 97.
FEATURES Location/Qualifiers
source 1. .97
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0225B12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 33 a 13 c 19 g 32 t
ORIGIN

Query Match 68.6%; Score 14.4; DB 17; Length 97;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4 TTTCTAGGAATTCAAA 19
           |||||||||||||| |
Db      21 TTTCTAGGAATTCACA 36
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RESULT 6
BH851999

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LOCUS       BH851999                 48 bp    DNA     linear   GSS 13-JUN-2002
DEFINITION  SALK_074019.36.90.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_074019.36.90.x, DNA
            sequence.
ACCESSION   BH851999
VERSION     BH851999.1  GI:21422870
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within 300 bases of the 5' end of
            At5g16310 and 300 bases of the 5' end of At5g16320.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_074019.36.90.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       12 a      4 c     12 g     20 t
ORIGIN

  Query Match           67.6%;  Score 14.2;  DB 17;  Length 48;
  Best Local Similarity  84.2%;  Pred. No. 2.5e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GATTTCTAGGAATTCAAAT 20
           ||||| ||| |||| ||||
Db      28 GATTTGTAGAAATTGAAAT 46


RESULT 7
BG153679/c
LOCUS       BG153679                 60 bp    mRNA    linear   EST 05-FEB-2001
DEFINITION  nag58g08.x1 NCI_CGAP_Co26 Homo sapiens cDNA clone IMAGE:4225743 3',
            mRNA sequence.
ACCESSION   BG153679
VERSION     BG153679.1  GI:12665709
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4225743"
                     /clone_lib="NCI_CGAP_Co26"
                     /tissue_type="normal colonic mucosa"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pAMP1; mRNA made from normal
                     colonic mucosa, cDNA made by oligo-dT priming.
                     Directionally cloned into UDG sites. Size-selected on
                     agarose gel,  average insert size 300 bp. Primary library.
                     cDNA Library Preparation:  David B. Krizman, Ph.D.
                     Reference: Krizman et al. (1996) Cancer Research
                     56:5380-5383."
BASE COUNT       17 a     17 c      9 g     17 t
ORIGIN

  Query Match           67.6%;  Score 14.2;  DB 12;  Length 60;
  Best Local Similarity  84.2%;  Pred. No. 2.5e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GATTTCTAGGAATTCAAAT 20
           || ||| ||||||||||  |
Db      20 GAATTCGAGGAATTCAAGT 2


RESULT 8
AI966296
LOCUS       AI966296                 83 bp    mRNA    linear   EST 30-NOV-2001
DEFINITION  sc36h04.y1 Gm-c1014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1014-1232 5', mRNA sequence.
ACCESSION   AI966296
VERSION     AI966296.1  GI:5760933
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 83)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .83
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
```

/clone="GENOME SYSTEMS CLONE ID: Gm-c1014-1232"
/clone_lib="Gm-c1014"
/tissue_type="Leaves, 2-3 week old seedlings, greenhouse grown"
/lab_host="DH10B"
/note="Vector: pT7T3Pac (pT7T3, Pharmacia); Site_1: EcoRI; Site_2: HindIII; This cDNA library was constructed from mRNA isolated from leaves of 2-3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a 3' anchored poly (dT) primer. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and HindIII. The cDNA fragments were directionally cloned into the EcoRI-HindIII restriction site of the pT7T3-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
BASE COUNT 32 a 9 c 8 g 34 t
ORIGIN

Query Match 67.6%; Score 14.2; DB 9; Length 83;
Best Local Similarity 84.2%; Pred. No. 2.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGATTTCTAGGAATTCAAA 19
| ||||| |||||||| ||
Db 12 AAATTTCAAGGAATTCGAA 30

RESULT 9
BJ077154/c
LOCUS BJ077154 47 bp mRNA linear EST 11-DEC-2001
DEFINITION BJ077154 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL060a15 3', mRNA sequence.
ACCESSION BJ077154
VERSION BJ077154.1 GI:17522070
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 47)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES Location/Qualifiers
source 1. .47
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL060a15"
/clone_lib="NIBB Mochii normalized Xenopus tailbud library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). "
BASE COUNT 9 a 3 c 9 g 22 t 4 others
ORIGIN

Query Match 65.7%; Score 13.8; DB 13; Length 47;
Best Local Similarity 88.2%; Pred. No. 3.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATTTCTAGGAATTCAAA 19
| |||||||||| ||||
Db 19 AGTTCTAGGAATCCAAA 3

RESULT 10
AA422541
LOCUS AA422541 49 bp mRNA linear EST 16-OCT-1997
DEFINITION vf14c03.s1 Knowles Solter mouse unfertilized egg Mus musculus cDNA clone IMAGE:835684 5', mRNA sequence.
ACCESSION AA422541
VERSION AA422541.1 GI:2101361
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 49)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:495900
Seq primer: -40m13 fwd. ET from Amersham.
FEATURES Location/Qualifiers
source 1. .49
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:835684"
/clone_lib="Knowles Solter mouse unfertilized egg"
/tissue_type="unfertilized egg"
/lab_host="DH10B"
/note="Organ: unfertilized egg; Vector: pBluescribe (modified); Site_1: MluI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 5000 unfertilized eggs. Primer: SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'. cDNAs were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.0 kb."
BASE COUNT 22 a 3 c 10 g 14 t
ORIGIN

Query Match 65.7%; Score 13.8; DB 9; Length 49;
Best Local Similarity 88.2%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATTTCTAGGAATTCAAA 19
| |||||||||| |||
Db 29 AGTTCTAGGAATTGAAA 45

RESULT 11
AZ810918/c
LOCUS AZ810918 69 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0076K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0076K14 R, DNA sequence.
ACCESSION AZ810918

```
VERSION     AZ810918.1  GI:12978657
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 69)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0076  row: K  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 69.
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0076K14"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       21 a     16 c     10 g     22 t
ORIGIN

  Query Match             65.7%;  Score 13.8;  DB 17;  Length 69;
  Best Local Similarity   88.2%;  Pred. No. 3.8e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 TTTCTAGGAATTCAAAT 20
           |||| ||||||| ||||
Db      27 TTTCAAGGAATTAAAAT 11


RESULT 12
AZ956832/c
LOCUS       AZ956832                69 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0223C05R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0223C05 R, DNA sequence.
ACCESSION   AZ956832
```

```
VERSION     AZ956832.1  GI:13828059
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 69)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0223  row: C  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 69.
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0223C05"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       18 a     19 c     11 g     21 t
ORIGIN

  Query Match             65.7%;  Score 13.8;  DB 17;  Length 69;
  Best Local Similarity   88.2%;  Pred. No. 3.8e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 AGATTTCTAGGAATTCA 17
           ||||| ||||| |||||
Db      18 AGATTACTAGGGATTCA 2


RESULT 13
BG153467/c
LOCUS       BG153467                76 bp    mRNA    linear   EST 05-FEB-2001
DEFINITION  nag49a01.x1 NCI_CGAP_Co29 Homo sapiens cDNA clone IMAGE:4204320 3',
            mRNA sequence.
ACCESSION   BG153467
```

```
VERSION     BG153467.1  GI:12665497
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 76)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .76
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4204320"
                     /clone_lib="NCI_CGAP_Co29"
                     /tissue_type="tubulovillous adenoma"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pAMP1; mRNA made from colonic
                     adenoma, cDNA made by oligo-dT priming.  Directionally
                     cloned into UDG sites. Size-selected on agarose gel,
                     average insert size 300 bp. Primary library. cDNA Library
                     Preparation:  David B. Krizman, Ph.D. Reference: Krizman
                     et al. (1996) Cancer Research  56:5380-5383."
BASE COUNT       22 a     20 c     14 g     20 t
ORIGIN

  Query Match             65.7%;  Score 13.8;  DB 12;  Length 76;
  Best Local Similarity   88.2%;  Pred. No. 3.8e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GATTTCTAGGAATTCAA 18
           || ||| ||||||||||
Db      24 GAATTCGAGGAATTCAA 8


RESULT 14
BG151684/c
LOCUS       BG151684                 82 bp    mRNA    linear   EST 05-FEB-2001
DEFINITION  nag63b11.x1 NCI_CGAP_Co26 Homo sapiens cDNA clone IMAGE:4226252 3',
            mRNA sequence.
ACCESSION   BG151684
VERSION     BG151684.1  GI:12663714
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 82)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .82
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4226252"
                     /clone_lib="NCI_CGAP_Co26"
                     /tissue_type="normal colonic mucosa"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pAMP1; mRNA made from normal
                     colonic mucosa, cDNA made by oligo-dT priming.
                     Directionally cloned into UDG sites. Size-selected on
                     agarose gel,  average insert size 300 bp. Primary library.
                     cDNA Library Preparation:  David B. Krizman, Ph.D.
                     Reference: Krizman et al. (1996) Cancer Research
                     56:5380-5383."
BASE COUNT       22 a     21 c     14 g     24 t      1 others
ORIGIN

  Query Match             65.7%;  Score 13.8;  DB 12;  Length 82;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GATTTCTAGGAATTCAA 18
           || ||| ||||||||||
Db      40 GAATTCGAGGAATTCAA 24


RESULT 15
BG151856/c
LOCUS       BG151856                 88 bp    mRNA    linear   EST 05-FEB-2001
DEFINITION  nag65d05.x1 NCI_CGAP_Co26 Homo sapiens cDNA clone IMAGE:4226360 3',
            mRNA sequence.
ACCESSION   BG151856
VERSION     BG151856.1  GI:12663886
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 88)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .88
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4226360"
                     /clone_lib="NCI_CGAP_Co26"
                     /tissue_type="normal colonic mucosa"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pAMP1; mRNA made from normal
                     colonic mucosa, cDNA made by oligo-dT priming.
                     Directionally cloned into UDG sites. Size-selected on
                     agarose gel,  average insert size 300 bp. Primary library.
                     cDNA Library Preparation:  David B. Krizman, Ph.D.
                     Reference: Krizman et al. (1996) Cancer Research
                     56:5380-5383."
BASE COUNT       23 a     23 c     17 g     25 t
ORIGIN

  Query Match             65.7%;  Score 13.8;  DB 12;  Length 88;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       2 GATTTCTAGGAATTCAA 18
           || ||| ||||||||||
Db      35 GAATTCGAGGAATTCAA 19
```

Search completed: December 25, 2002, 12:30:48
Job time : 2991 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 14:02:35 ; Search time 54 Seconds
(without alignments)
67.706 Million cell updates/sec

Title: SCHMIDT875
Perfect score: 9
Sequence: 1 ttcnnngaa 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 221248

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	66.7	9	9	US-10-136-224-13	Sequence 13, Appl
c	2	6	66.7	9	9	US-10-136-224-13	Sequence 13, Appl
	3	6	66.7	9	10	US-09-842-761-4	Sequence 4, Appli
c	4	6	66.7	9	10	US-09-842-761-4	Sequence 4, Appli
	5	6	66.7	9	10	US-09-816-763-112	Sequence 112, App
c	6	6	66.7	9	10	US-09-816-763-112	Sequence 112, App
	7	6	66.7	11	9	US-10-113-877-21	Sequence 21, Appl
c	8	6	66.7	11	9	US-10-113-877-21	Sequence 21, Appl
	9	6	66.7	11	9	US-10-113-877-25	Sequence 25, Appl
c	10	6	66.7	11	9	US-10-113-877-25	Sequence 25, Appl
	11	6	66.7	12	9	US-10-113-877-23	Sequence 23, Appl
c	12	6	66.7	12	9	US-10-113-877-23	Sequence 23, Appl
	13	6	66.7	12	9	US-10-113-877-24	Sequence 24, Appl
c	14	6	66.7	12	9	US-10-113-877-24	Sequence 24, Appl
	15	6	66.7	15	10	US-09-504-231A-366	Sequence 366, App
c	16	6	66.7	15	10	US-09-504-231A-366	Sequence 366, App
	17	6	66.7	15	10	US-09-504-231A-367	Sequence 367, App
c	18	6	66.7	15	10	US-09-504-231A-367	Sequence 367, App
	19	6	66.7	15	10	US-09-504-231A-935	Sequence 935, App
c	20	6	66.7	15	10	US-09-504-231A-935	Sequence 935, App
	21	6	66.7	15	10	US-09-504-231A-936	Sequence 936, App
c	22	6	66.7	15	10	US-09-504-231A-936	Sequence 936, App
	23	6	66.7	15	10	US-09-504-231A-981	Sequence 981, App
c	24	6	66.7	15	10	US-09-504-231A-981	Sequence 981, App
	25	6	66.7	15	10	US-09-504-231A-982	Sequence 982, App
c	26	6	66.7	15	10	US-09-504-231A-982	Sequence 982, App
	27	6	66.7	15	10	US-09-504-231A-1096	Sequence 1096, Ap
c	28	6	66.7	15	10	US-09-504-231A-1096	Sequence 1096, Ap
	29	6	66.7	15	10	US-09-504-231A-1097	Sequence 1097, Ap
c	30	6	66.7	15	10	US-09-504-231A-1097	Sequence 1097, Ap
	31	6	66.7	15	10	US-09-504-231A-1098	Sequence 1098, Ap
c	32	6	66.7	15	10	US-09-504-231A-1098	Sequence 1098, Ap
	33	6	66.7	15	10	US-09-274-553D-366	Sequence 366, App
c	34	6	66.7	15	10	US-09-274-553D-366	Sequence 366, App
	35	6	66.7	15	10	US-09-274-553D-367	Sequence 367, App
c	36	6	66.7	15	10	US-09-274-553D-367	Sequence 367, App
	37	6	66.7	15	10	US-09-274-553D-935	Sequence 935, App
c	38	6	66.7	15	10	US-09-274-553D-935	Sequence 935, App
	39	6	66.7	15	10	US-09-274-553D-936	Sequence 936, App
c	40	6	66.7	15	10	US-09-274-553D-936	Sequence 936, App
	41	6	66.7	15	10	US-09-274-553D-981	Sequence 981, App
c	42	6	66.7	15	10	US-09-274-553D-981	Sequence 981, App
	43	6	66.7	15	10	US-09-274-553D-982	Sequence 982, App
c	44	6	66.7	15	10	US-09-274-553D-982	Sequence 982, App
	45	6	66.7	15	10	US-09-274-553D-1096	Sequence 1096, Ap

ALIGNMENTS

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RESULT 1
US-10-136-224-13
; Sequence 13, Application US/10136224
; Patent No. US20020174448A1
; GENERAL INFORMATION:
;  APPLICANT: AUERNHAMMER, CHRISTOPH J.
;  APPLICANT:  MELMED, SHLOMO
;  TITLE OF INVENTION: SUPPRESSOR OF CYTOKINE SIGNALING
;  TITLE OF INVENTION:  (SOCS)-3 PROMOTER AND METHODS FOR ITS USE IN GENETIC THERAPY
;  TITLE OF INVENTION:  IN HUMANS
;  FILE REFERENCE: P07 42591
;  CURRENT APPLICATION NUMBER: US/10/136,224
;  CURRENT FILING DATE:  2002-04-29
;  PRIOR APPLICATION NUMBER: US/09/327,138
;  PRIOR FILING DATE: 1999-06-07
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: MURINE
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (-74)...(-66)
;   OTHER INFORMATION: STAT-BINDING SITE AT -74 TO -66
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (0)...(0)
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: STAT-BINDING SITE AT -74 TO 66
US-10-136-224-13

  Query Match             66.7%;  Score 6;  DB 9;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 4.3e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       1 TTCCAGGAA 9
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RESULT 2
US-10-136-224-13/c
; Sequence 13, Application US/10136224
; Patent No. US20020174448A1
; GENERAL INFORMATION:
;  APPLICANT: AUERNHAMMER, CHRISTOPH J.
;  APPLICANT:  MELMED, SHLOMO
;  TITLE OF INVENTION: SUPPRESSOR OF CYTOKINE SIGNALING
;  TITLE OF INVENTION:  (SOCS)-3 PROMOTER AND METHODS FOR ITS USE IN GENETIC THERAPY
;  TITLE OF INVENTION:  IN HUMANS
;  FILE REFERENCE: P07 42591
;  CURRENT APPLICATION NUMBER: US/10/136,224
;  CURRENT FILING DATE:  2002-04-29
;  PRIOR APPLICATION NUMBER: US/09/327,138
;  PRIOR FILING DATE: 1999-06-07
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: MURINE
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (-74)...(-66)
;   OTHER INFORMATION: STAT-BINDING SITE AT -74 TO -66
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (0)...(0)
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: STAT-BINDING SITE AT -74 TO 66
US-10-136-224-13

  Query Match            66.7%;  Score 6;  DB 9;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 4.3e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCCTGGAA 1


RESULT 3
US-09-842-761-4
; Sequence 4, Application US/09842761
; Patent No. US20020081602A1
; GENERAL INFORMATION:
;  APPLICANT: Beeley, Lee
;  TITLE OF INVENTION: Method for the Detection of Compounds
;  TITLE OF INVENTION:  that Modulate the Effects of the Obese (OB) Protein
;  FILE REFERENCE: P31648-C1
;  CURRENT APPLICATION NUMBER: US/09/842,761
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 09/297,442
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-842-761-4

  Query Match            66.7%;  Score 6;  DB 10;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 4.3e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCCCGGAA 9


RESULT 4
US-09-842-761-4/c
; Sequence 4, Application US/09842761
; Patent No. US20020081602A1
; GENERAL INFORMATION:
;  APPLICANT: Beeley, Lee
;  TITLE OF INVENTION: Method for the Detection of Compounds
;  TITLE OF INVENTION:  that Modulate the Effects of the Obese (OB) Protein
;  FILE REFERENCE: P31648-C1
;  CURRENT APPLICATION NUMBER: US/09/842,761
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 09/297,442
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-842-761-4

  Query Match            66.7%;  Score 6;  DB 10;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 4.3e+07;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCCGGGAA 1


RESULT 5
US-09-816-763-112
; Sequence 112, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
;  APPLICANT: Remacle, Jose
;  APPLICANT:  Renard, Patricia
;  APPLICANT:  Art, Muriel
;  TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
;  TITLE OF INVENTION:  DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
;  TITLE OF INVENTION:  FACTORS
;  FILE REFERENCE: VANM212.001AUS
;  CURRENT APPLICATION NUMBER: US/09/816,763
;  CURRENT FILING DATE:  2001-03-23
;  PRIOR APPLICATION NUMBER: EP 00870057.7
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus sequence for transcriptional factor STAT
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(9)
;   OTHER INFORMATION: n = A,T,C or G
US-09-816-763-112

  Query Match            66.7%;  Score 6;  DB 10;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 4.3e+07;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||||||||
Db      1 TTCNNNGAA 9


RESULT 6
US-09-816-763-112/c
; Sequence 112, Application US/09816763
; Patent No. US20020110814A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Remacle, Jose
;  APPLICANT:  Renard, Patricia
;  APPLICANT:  Art, Muriel
;  TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
;  TITLE OF INVENTION:  DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
;  TITLE OF INVENTION:  FACTORS
;  FILE REFERENCE: VANM212.001AUS
;  CURRENT APPLICATION NUMBER: US/09/816,763
;  CURRENT FILING DATE:  2001-03-23
;  PRIOR APPLICATION NUMBER: EP 00870057.7
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus sequence for transcriptional factor STAT
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(9)
;   OTHER INFORMATION: n = A,T,C or G
US-09-816-763-112

  Query Match            66.7%;  Score 6;  DB 10;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+07;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||||||||
Db      9 TTCNNNGAA 1


RESULT 7
US-10-113-877-21
; Sequence 21, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-21

  Query Match            66.7%;  Score 6;  DB 9;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+04;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      1 TTCTGGGAA 9


RESULT 8
US-10-113-877-21/c
; Sequence 21, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-21

  Query Match            66.7%;  Score 6;  DB 9;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+04;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      9 TTCCCAGAA 1


RESULT 9
US-10-113-877-25
; Sequence 25, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-25

  Query Match            66.7%;  Score 6;  DB 9;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+04;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      2 TTCCCAGAA 10


RESULT 10
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US-10-113-877-25/c
; Sequence 25, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-25

  Query Match             66.7%;  Score 6;  DB 9;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+04;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db     10 TTCTGGGAA 2


RESULT 11
US-10-113-877-23
; Sequence 23, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-23

  Query Match             66.7%;  Score 6;  DB 9;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+04;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      2 TTCCCCGAA 10
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```
RESULT 12
US-10-113-877-23/c
; Sequence 23, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-23

  Query Match             66.7%;  Score 6;  DB 9;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+04;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db     10 TTCGGGGAA 2


RESULT 13
US-10-113-877-24
; Sequence 24, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-24

  Query Match             66.7%;  Score 6;  DB 9;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+04;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 TTCNNNGAA 9
          |||   |||
Db      2 TTCTTTGAA 10
```

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RESULT 14
US-10-113-877-24/c
; Sequence 24, Application US/10113877
; Patent No. US20020177218A1
; GENERAL INFORMATION:
;  APPLICANT: Fang, Yu
;  APPLICANT:  Wang, Xiao-Yang
;  APPLICANT:  Turpin, Pierre
;  TITLE OF INVENTION: Methods of detecting multiple DNA
;  TITLE OF INVENTION:  binding protein and DNA interactions in a sample, and
;  TITLE OF INVENTION:  devices, systems and kits for practicing the same.
;  FILE REFERENCE: CLON-071
;  CURRENT APPLICATION NUMBER: US/10/113,877
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: 60/280,658
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 60/314,330
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-113-877-24

  Query Match            66.7%;  Score 6;  DB 9;  Length 12;
  Best Local Similarity  66.7%;  Pred. No. 2.9e+04;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db      10 TTCAAAGAA 2


RESULT 15
US-09-504-231A-366
; Sequence 366, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 366
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-504-231A-366

  Query Match            66.7%;  Score 6;  DB 10;  Length 15;
  Best Local Similarity  44.4%;  Pred. No. 3e+04;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            ::|   |||
Db       7 UUCACCGAA 15


Search completed: December 25, 2002, 22:45:49
Job time : 55 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2002, 12:30:59 ; Search time 1971 Seconds
(without alignments)
73.952 Million cell updates/sec

Title: SCHMIDT875
Perfect score: 9
Sequence: 1 ttcnnngaa 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	66.7	19	17	AZ835621	AZ835621 2M0129L21
c	2	6	66.7	19	17	AZ835621	AZ835621 2M0129L21
	3	6	66.7	20	13	BM400102	BM400102 5009-0-66
c	4	6	66.7	20	13	BM400102	BM400102 5009-0-66
	5	6	66.7	21	17	AZ360212	AZ360212 1M0103K04
c	6	6	66.7	21	17	AZ360212	AZ360212 1M0103K04
	7	6	66.7	21	17	AZ484782	AZ484782 1M0311C05
c	8	6	66.7	21	17	AZ484782	AZ484782 1M0311C05
	9	6	66.7	22	17	AZ430664	AZ430664 1M0215D17
c	10	6	66.7	22	17	AZ430664	AZ430664 1M0215D17
	11	6	66.7	22	17	AZ508843	AZ508843 1M0351E06
c	12	6	66.7	22	17	AZ508843	AZ508843 1M0351E06
	13	6	66.7	22	17	AZ816374	AZ816374 2M0085O05
c	14	6	66.7	22	17	AZ816374	AZ816374 2M0085O05
	15	6	66.7	22	17	TA196G02P	AL475949 T. brucei
c	16	6	66.7	22	17	TA196G02P	AL475949 T. brucei
	17	6	66.7	23	9	AU012492	AU012492 AU012492
c	18	6	66.7	23	9	AU012492	AU012492 AU012492
	19	6	66.7	23	17	AZ305600	AZ305600 1M0006A19
c	20	6	66.7	23	17	AZ305600	AZ305600 1M0006A19
	21	6	66.7	23	17	AZ388663	AZ388663 1M0148J15
c	22	6	66.7	23	17	AZ388663	AZ388663 1M0148J15
	23	6	66.7	23	17	AZ424145	AZ424145 1M0203P03
c	24	6	66.7	23	17	AZ424145	AZ424145 1M0203P03
	25	6	66.7	23	17	AZ847801	AZ847801 2M0148G06
c	26	6	66.7	23	17	AZ847801	AZ847801 2M0148G06
	27	6	66.7	24	14	L32040	L32040 HUMXP2D9A H
c	28	6	66.7	24	14	L32040	L32040 HUMXP2D9A H
	29	6	66.7	24	17	AZ357286	AZ357286 1M0098B15
c	30	6	66.7	24	17	AZ357286	AZ357286 1M0098B15
	31	6	66.7	24	17	AZ829302	AZ829302 2M0106G20
c	32	6	66.7	24	17	AZ829302	AZ829302 2M0106G20
	33	6	66.7	24	17	TA196H02P	AL475956 T. brucei
c	34	6	66.7	24	17	TA196H02P	AL475956 T. brucei
	35	6	66.7	24	17	TA256C04P	AL482493 T. brucei
c	36	6	66.7	24	17	TA256C04P	AL482493 T. brucei
	37	6	66.7	24	17	TA273G07Q	AL487649 T. brucei
c	38	6	66.7	24	17	TA273G07Q	AL487649 T. brucei
	39	6	66.7	25	9	AI247983	AI247983 qh63b01.x
c	40	6	66.7	25	9	AI247983	AI247983 qh63b01.x
	41	6	66.7	25	17	BH863680	BH863680 SALK_0943
c	42	6	66.7	25	17	BH863680	BH863680 SALK_0943
	43	6	66.7	26	17	AZ822697	AZ822697 2M0096I07
c	44	6	66.7	26	17	AZ822697	AZ822697 2M0096I07
	45	6	66.7	27	14	L32053	L32053 HUMXP519A H

ALIGNMENTS

RESULT 1
AZ835621
LOCUS AZ835621 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0129L21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0129L21 R, DNA sequence.
ACCESSION AZ835621
VERSION AZ835621.1 GI:13005529
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

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            Plate: 0129  row: L  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0129L21"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        6 a      3 c      3 g      7 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 4.4e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db       2 TTCTGTGAA 10


RESULT 2
AZ835621/c
LOCUS       AZ835621                 19 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0129L21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0129L21 R, DNA sequence.
ACCESSION   AZ835621
VERSION     AZ835621.1  GI:13005529
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0129  row: L  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0129L21"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT        6 a      3 c      3 g      7 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 4.4e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db      10 TTCACAGAA 2


RESULT 3
BM400102
LOCUS       BM400102                 20 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-66-D02.t.2 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM400102
VERSION     BM400102.1  GI:18200155
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Tetrahymena thermophila"
                      /strain="CU428.1"
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                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT        4 a      3 c      8 g      5 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 13;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db      12 TTCGGGGAA 20


RESULT 4
BM400102/c
LOCUS       BM400102                 20 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-66-D02.t.2 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM400102
VERSION     BM400102.1  GI:18200155
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT        4 a      3 c      8 g      5 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 13;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db      20 TTCCCCGAA 12


RESULT 5
AZ360212
LOCUS       AZ360212                 21 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0103K04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0103K04 F, DNA sequence.
ACCESSION   AZ360212
VERSION     AZ360212.1  GI:10473912
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: K  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0103K04"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      7 c      5 g      3 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
           |||   |||
Db       7 TTCTGGGAA 15


RESULT 6
AZ360212/c
LOCUS       AZ360212                 21 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0103K04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0103K04 F, DNA sequence.
ACCESSION   AZ360212
VERSION     AZ360212.1  GI:10473912
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: K  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0103K04"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      7 c      5 g      3 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db      15 TTCCCAGAA 7


RESULT 7
AZ484782
LOCUS       AZ484782                 21 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0311C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0311C05 R, DNA sequence.
ACCESSION   AZ484782
VERSION     AZ484782.1  GI:10649960
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0311  row: C  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0311C05"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        7 a      3 c      4 g      7 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       1 TTCGGTGAA 9


RESULT 8
AZ484782/c
LOCUS       AZ484782                 21 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0311C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0311C05 R, DNA sequence.
ACCESSION   AZ484782
VERSION     AZ484782.1  GI:10649960
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0311  row: C  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0311C05"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        7 a      3 c      4 g      7 t
ORIGIN

  Query Match            66.7%;  Score 6;  DB 17;  Length 21;
  Best Local Similarity  66.7%;  Pred. No. 4.5e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       9 TTCACCGAA 1


RESULT 9
AZ430664
LOCUS       AZ430664                 22 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0215D17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0215D17 F, DNA sequence.
ACCESSION   AZ430664
VERSION     AZ430664.1  GI:10554677
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0215  row: D  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0215D17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      4 c      3 g      9 t
ORIGIN

  Query Match            66.7%;  Score 6;  DB 17;  Length 22;
  Best Local Similarity  66.7%;  Pred. No. 4.6e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db      13 TTCTGGGAA 21


RESULT 10
AZ430664/c
LOCUS       AZ430664                 22 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0215D17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0215D17 F, DNA sequence.
ACCESSION   AZ430664
VERSION     AZ430664.1  GI:10554677
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
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```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0215  row: D  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0215D17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      4 c      3 g      9 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 22;
  Best Local Similarity   66.7%;  Pred. No. 4.6e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db      21 TTCCCAGAA 13


RESULT 11
AZ508843
LOCUS       AZ508843                 22 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0351E06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0351E06 R, DNA sequence.
ACCESSION   AZ508843
VERSION     AZ508843.1  GI:10690159
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0351  row: E  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0351E06"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      5 c      3 g      8 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 22;
  Best Local Similarity   66.7%;  Pred. No. 4.6e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       7 TTCAGTGAA 15


RESULT 12
AZ508843/c
LOCUS       AZ508843                 22 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0351E06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0351E06 R, DNA sequence.
ACCESSION   AZ508843
VERSION     AZ508843.1  GI:10690159
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0351  row: E  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0351E06"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        6 a      5 c      3 g      8 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 22;
  Best Local Similarity   66.7%;  Pred. No. 4.6e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db      15 TTCACTGAA 7


RESULT 13
AZ816374
LOCUS       AZ816374                 22 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0085O05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0085O05 F, DNA sequence.
ACCESSION   AZ816374
VERSION     AZ816374.1  GI:12986282
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0085  row: O  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0085O05"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        8 a      2 c      8 g      4 t
ORIGIN

  Query Match             66.7%;  Score 6;  DB 17;  Length 22;
  Best Local Similarity   66.7%;  Pred. No. 4.6e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 TTCNNNGAA 9
            |||   |||
Db       3 TTCTAGGAA 11


RESULT 14
AZ816374/c
LOCUS       AZ816374                 22 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0085O05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0085O05 F, DNA sequence.
ACCESSION   AZ816374
VERSION     AZ816374.1  GI:12986282
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: O column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0085O05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 2 c 8 g 4 t
ORIGIN

Query Match 66.7%; Score 6; DB 17; Length 22;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTCNNNGAA 9
||| |||
Db 11 TTCCTAGAA 3

RESULT 15
TA196G02P
LOCUS TA196G02P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 196g02, forward sequence, genomic survey sequence.
ACCESSION AL475949
VERSION AL475949.1 GI:11842689
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers
source 1. .22
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="196g02"

BASE COUNT 4 a 5 c 6 g 7 t
ORIGIN

Query Match 66.7%; Score 6; DB 17; Length 22;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTCNNNGAA 9
||| |||
Db 2 TTCTCTGAA 10

Search completed: December 25, 2002, 20:55:16
Job time : 1977 secs